

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 22:28:26 ; Search time 7449 Seconds
(without alignments)

10810.020 Million cell updates/sec

Title: US-10-678-023a-1

Perfect score: 1439.2

Sequence: 1 tggagagttgatcctggct.....agaagtggtaggtaaccg 1440

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_est7:*
- 7: gb_est8:*
- 8: gb_est9:*
- 9: gb_est10:*
- 10: gb_est11:*
- 11: gb_est12:*
- 12: gb_est13:*
- 13: gb_est14:*
- 14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	799.8	55.6	6499	11	BH771024
2	716.8	49.8	1954	8	CX109203
C 3	655.4	45.5	793	13	DU370470
4	633.2	44.0	941	5	CK296497
5	615.8	42.8	1084	11	BZ439740
C 6	613.8	42.6	1053	11	BZ447500
C 7	608	42.2	1010	11	BZ431523
8	602.8	41.9	1033	14	DU743187
C 9	602.4	41.9	1016	11	BZ426201
10	599.4	41.6	889	5	CK280527
C 11	599.4	41.6	1143	11	BH814966
12	599	41.6	1079	11	BH705272
C 13	595.8	41.4	976	14	DU733613
14	592.8	41.2	884	5	CK280528
15	592.8	41.2	917	14	DU476609
C 16	591	41.1	1031	11	BH656222
C 17	585.4	40.7	1044	11	BZ463550
C 18	585.4	40.7	1051	11	BZ494182
C 19	584.8	40.6	899	12	BZ685785

20	581.2	40.4	1077	11	BZ450751
21	576	40.0	861	14	DU486180
22	573	39.8	746	11	AQ957362
23	572.8	39.8	787	8	COL59272
24	568	39.5	845	14	DU477585
25	566.8	39.4	863	14	DU487250
26	564.6	39.2	840	14	DU478845
27	563	39.1	974	11	BZ440868
28	560.8	39.0	810	14	DU477669
29	560.2	38.9	854	14	DU477664
C 30	558.8	38.8	716	11	AQ957363
C 31	558.4	38.8	1054	11	BH647750
C 32	558	38.8	894	14	DU487242
33	554.6	38.5	830	14	DU476605
C 34	552.8	38.4	890	14	DU476594
C 35	552.6	38.4	756	9	DN469396
36	552.6	38.4	851	5	CK290947
C 37	550.6	38.3	1106	11	BZ469058
38	549.4	38.2	860	8	CN757363
C 39	547.2	38.0	1069	11	BZ474941
C 40	545.8	37.9	924	13	DU101928
41	543.4	37.8	951	11	BH651765
C 42	540.2	37.5	957	14	DU744805
43	540	37.5	817	14	DU477671
C 44	537.8	37.4	861	14	DU486177
45	537.4	37.3	977	11	BZ459292

ALIGNMENTS

RESULT 1
LOCUS BH771024 6499 bp DNA linear GSS 01-MAY-2002
DEFINITION LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH771024
VERSION BH771024.1 GI:20373981
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin A., Ehrlich S.D. and Sorokin A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is ywGA (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
Location/Qualifiers
1. .6499
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="cremoris"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGM2; Site 1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."

ORIGIN

Query Match 55.6%; Score 799.8; DB 11; Length 6499;
Best Local Similarity 76.0%; Pred. No. 1.7e-234;

Matches 1106; Conservative 1; Mismatches 329; Indels 19; Gaps 9;									
Qy	1	TGGAGAGTTTGATCCTCGCTCAGATTGAA	CGCTGGCGGCATGCTTTACATGCAAGTCG	60					
Db	529	TTGAGAGTTTGATCCTCGCTCAGGACGAA	CGCTGGCGGCATGCTTTACATGCAAGTCG	588					
Qy	61	AACG--GTAAACAGAGTCTTGCACCC--	GCTACACAGTGGCGAAGCGGTGAGTAAGTGGT-	115					
Db	589	AGCGATGAAGATTGGTGGCTTGCACAAAT	TGAAGAGCAGCGAAGCGGTGAGTAAGTGGT	648					
Qy	116	CGGAATGTACCGTGAATGGGGGATAGCT	CGCGGAAAGCCGATTAATACCGCATACGCC	175					
Db	649	GGGAATCTGCCCTTTGAGCGGGGACAACT	TGGAACGAATGCTAATACCGCATATAA	708					
Qy	176	CT-----GAGGGGAAAGCGGGGATCG	AAAGACCTCGGTTATACGAGCAGCCGACG	228					
Db	709	CTTTAAACATAAAGTTTAAAGTTTAAAG	TGAAAGATGCAATTCACCTCAAAGATGATCCCGCG	768					
Qy	229	TCTGATTAGCTAGTTGGTGAAGTAAGAG	CTCACCAGCGCAGATCAGTAGCGGTCCTGA	288					
Db	769	TTGTATTAGCTAGTTGGTGAAGTAAGAG	CTCACCAGCGCAGATCAGTAGCGGTCCTGA	828					
Qy	289	GAGGATGATCGCCACACTCGGACTGAG	ACACGCGCCAGACTCTCTACGGGAGGCGAGT	348					
Db	829	GAGGATGATCGCCACACTCGGACTGAG	ACACGCGCCAGACTCTCTACGGGAGGCGAGT	888					
Qy	349	GGGGAATTTTGGACAAATGGGGGCAAC	CTGATCAGCCATGCCCGTGTCTGAAGAAGGC	408					
Db	889	AGGGAATCTTCGGCAATGGACAAAGTCT	GACCGAGCAACCGCCGCTGAGTGAAGAAGGT	948					
Qy	409	CTTCGGGTGTAAAGGACTTTTGTTCAG	GGGGAATAATCCCGTGTGTAATATCCCGCGGGG	468					
Db	949	TTTCGGATCGTAATAACTCTGTGTGTA	GAGAAGACGTTGTGAGAGTGGAAGCTCATCA	1008					
Qy	469	A-TGACAGTACCBGAAGAATAAGCAC	CGCGCTAACTACGTGCACAGCCGCGTAAATACG	527					
Db	1009	AGTGACGTAATACTCCCAAGAAAGGAG	CGCGCTAACTACGTGCACAGCCGCGTAAATACG	1068					
Qy	528	TAGGTCGACGCTTAATCGGAATTACT	TGGCGGTAAAGCGTGCAGCGGCTTTTGAAG	587					
Db	1069	TAGTCCCGAGCGTTGTCCGAATTTAT	TGGCGGTAAAGCGTGCAGCGGCTTTTGAAG	1128					
Qy	588	TCTGATGTAAAGCCCGCGCTCAACCT	TGGGAAACGGCATTCGAGACTGCAAGACTAGAGT	647					
Db	1129	TCTGATGTAAAGCGAGTGGCTCAACC	ATTGTA-TGCATTGGAACCTGCTAGACTTAGT	1187					
Qy	648	CGCTCAGAGGGGGTAGAATTCGCGTG	TAGCAGTGAATCCGTAGAGATCCGAGGAAT	707					
Db	1188	GCAGGAGAGGAGTGGAAATTCATGTG	TAGCGGTGAAATCGCTAGATATATCGAGGAAC	1247					
Qy	708	ACCGATGCGAAGCAGCGCCCTCGGAT	GACACTGACGCTCATGACGAAAGCGTGGGA	767					
Db	1248	ACCGGTGCGAAGCAGCGCTCTCTGCG	CTGTAACTGACACTGAGGCTCGAAAGCGTGGGA	1307					
Qy	768	GCAACACGATTAGATACCTGGTAGT	CCACCGCTTAAACGATGCTCAATTAGCTGTTGGG	827					
Db	1308	GCAACACGATTAGATACCTGGTAGT	CCACCGCTTAAACGATGCTAGTGTAGTAGG	1367					
Qy	828	-GGTTTGAATCCTTGGTAGCGTAGCT	AACCGGTGAAATTTGACCGCTGGGAGTACCGCC	886					
Db	1368	AGCTATAAGTTCTCTGTATCGCAGCT	AACGCAATAAGCACTCCGCTGGGAGTACGACC	1427					
Qy	887	GCNAGTTAAACTCAAGGAATTGACGG	GACCGCCGACAGCGGTGATGATGCGATT	946					
Db	1428	GCNAGTTGAAACTCAAGGAATTGACGG	GACCGCCGACAGCGGTGATGATGCGATT	1487					
Qy	947	AATTCGATGCAACCGGAAACCTTAC	CTGCTCTTGATCATGTAGC-GAACTTGGTAGAGA	1005					
Db	1488	AATTCGATGCAACCGGAAACCTTAC	CTGCTCTTGATCATGTAGC-GAACTTGGTAGAGA	1547					
Qy	1006	TATCTTGTGCGCCGAAAGGGAGCCG	TAAACAGGTGCTGCATGGCTGTCAGTCGCTG	1065					
Db	1548	TA---GGAAGTTTCTTTCGGGACACG	GGAATACAGGTGGTGCATGGTTGTCGTCAGCTCGT	1604					

Qy	1066	TCTGTGAGATGTTGGGTTAAGTCCCG	CAACGAGCGCAACCTTCTCATTTAGTTGCCATCAT	1125
Db	1605	TCTGTGAGATGTTGGGTTAAGTCCCG	CAACGAGCGCAACCTTCTCATTTAGTTGCCATCAT	1664
Qy	1126	TTAGTTGGGCACCTCTAATGAGACT	CGCGGTGACAAACCGGAGGAAGTGGGGATGACGTC	1185
Db	1665	TAAGTTGGGCACCTCTAACGAGACT	CGCGGTGATAAACCGGAGGAAGTGGGGATGACGTC	1724
Qy	1186	AAGTCTCATGCGCCCTTATGAGCAG	GGCTTTCACACGCTCATCAATGGTCCGTTACAGAGG	1245
Db	1725	AAATCATCATGCCCTTATGACCTGG	CGCTTACACAGCTGCTTACAAATGGATGGTACAACGAG	1784
Qy	1246	TCCCTAAGCGCGAGCTGGTGGCAAT	CTCATATAAACCGATCGTAGTCCGGATCGCACTCT	1305
Db	1785	TCGCGAGACAGTATGTTAGCTAA	TCTCTTAAACCATTTCTCAGTTCGGATTGTAGGCT	1844
Qy	1306	GCAACTCGAGTGGCGTGAAGTCG	GAATCGCTAGTAATCGCAGATCAGCATGCTCGCGTGAA	1365
Db	1845	GCAACTCGCTACATGAAGTCGGA	ATCGCTAGTAATCGCGGATCAGCAGCGCGGTGAA	1904
Qy	1366	TAGTTCCCGGGTCTTGTACACACC	CGCGCTACACCATGGGAGTGTTCACCCAGAG	1425
Db	1905	TACGTTCCCGGGCTTGTACACACC	CGCGCTACACCATGGGAGTGTTCACCCAGAG	1964
Qy	1426	TGGGTAGGCTAACCG	1440	
Db	1965	TAGTTGCTTAACCG	1979	
RESULT 2				
CX109203				
LOCUS				
DEFINITION				
RCM0593 A normalized whole-life-cycle cDNA library of rice Oryza				
sativa (indica cultivar-group) cDNA clone EI051022, EI053008,				
EI008B17, BI076L19, BI154A06, BI133B10, EI11 5', mRNA sequence.				
CX109203				
VERSION				
CX109203.1 GI:66922355				
KEYWORDS				
EST.				
SOURCE				
ORGANISM				
Oryza sativa (indica cultivar-group)				
Oryza sativa (indica cultivar-group)				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP				
clade; Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE				
AUTHORS				
Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D.,				
Han,B., Zhang,Q. and Wang,S.				
TITLE				
Features of the expressed sequences revealed by a large-scale				
analysis of ESTs from a normalized cDNA library of the elite indica				
rice cultivar Minghui 63				
JOURNAL				
PUBLISHED				
COMMENT				
Contact: Wang S				
National Key Laboratory of Crop Genetic Improvement				
Hauzhong Agricultural University				
Wuhan 430070, China				
Tel: 86-27-87282044				
Fax: 86-27-87287092				
Email: shiyingwang@hotmail.com				
Seq primer: T7.				
FEATURES				
source				
1..1954				
/organism="Oryza sativa (indica cultivar-group)"				
/mol_type="mRNA"				
/strain="indica"				
/cultivar="Minghui 63"				
/db_xref="taxon:39946"				
/clone="EI051022, EI053J08, EI008B17, BI076L19, BI154A06,				
BI133B10, EI11"				
/tissue_type="whole plant"				
/dev_stage="whole-life-cycle"				
/lab_host="E. coli DH10B"				
/clone_lib="A normalized whole-life-cycle cDNA library of				

rice"
/note="vector: psPort1; Site 1: Sali; Site 2: NotI; The
library is constructed based on the strategy of saturation
hybridization with genomic DNA using rice cultivar Minghui
63. This library consists of cDNA from 15 directionally
cloned cDNA libraries constructed with different tissues
from 9 developmental stages."

ORIGIN

Query Match	49.8%;	Score	716.8;	DB	8;	Length	1954;
Best Local Similarity	73.3%;	Pred. No.	4.7e-209;				
Matches 1059;	Conservative	1;	Mismatches 329;	Indels	55;	Gaps	9;
QY	1	TGAGAGTTTGTATCTCGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCG	60				
Db	105	TGAGAGATTGATCTCTGGCTTCAGATGAAAGCTGGCGGCATGCTTTACACATGCAAGTCG	164				
QY	61	AACGGTAAACAGGTTGCTTGCACCGCTGACGAGTGGCGAAGCGGTGAGTAATACCGCATACGCCCTGAG	180				
Db	165	AACGGGAAGTGG-----TGTTTCAGTGGCGAAACGGGTGAGTACCGGTAAAGAA	213				
QY	121	TGTACCGTGTAAATGGGGGATAGCTCGCGGAAAGCCGGATTAATACCGCATACGCCCTGAG	271				
Db	214	CTTGCCCTTTGGGAGGGGAAACAACACTGGAACCGTTGCTTAATACCCCGTAGG--CTGAG	271				
QY	181	GGGGAAGCGGGGATCGAAAGACCTCGCGTTATACGAGCAGCGGACGCTCTGATTAGCTA	240				
Db	272	GAGCAAAAGGAGAAATC-----CGCCCAAGAGGGGCTCGGCTCTGATTAGCTA	320				
QY	241	GTGGTGAAGTAAGAGTCTCAACGAGGCGACGATCAGTAGCGGCTCTGAGAGGATGATCCG	300				
Db	321	GTGGTGAAGCAATAGTCTTACCAAGGCGATGATCAGTAGCTGTTCCGAGAGGATGATCAG	380				
QY	301	CCACACTGGGACTGAGACACGGCCAGACTCTTACGGAGCGCAGCAGTGGGGAATTTTGG	360				
Db	381	CCACACTGGGACTGAGACACGGCCAGACTCTTACGGAGCGCAGCAGTGGGGAATTTTCC	440				
QY	361	ACAATGGGGCAACCTGATCCAGCCATGCGCGTGTCTGAAGAAGGCCCTTCGGGTGTA	420				
Db	441	GCAATGGGCGAAAGCTTGACGGAGCAATGCGCGTGGAGTGAAGGCCCAACGGGTCGTC	500				
QY	421	AAGGACTTTTGTGAGGAGGAAATCCCGCTGGTTAATACCCGCGGGGATGACAGTACCB	480				
Db	501	AACCTCTTTCTCGGAGAAGAAACA-----ATGACGGTATCT	537				
QY	481	GAGAAATAGCAGCCGCTAACTAGTCCAGCAGCGCGGTAAATACGTAGGTGCAAGCG	540				
Db	538	GAGGAAATAGCAGTCGGCTAACTCTGTGCCAGCAGCCGCGTAAAGAGAGATGCAAGCG	597				
QY	541	TTAATCGGAATTAAGTGGCGTAAAGCGTGGCGAGCGGTTTTCGAAGTCTGATGTGAAG	600				
Db	598	TTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGTGGCTTTTCAAGTCCCGCTCAAT	657				
QY	601	CCCCGGGCTCAACTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTGGCTCAGAGGGG	660				
Db	658	CCCAGGGCTCAACCTCGGACAGCGGTGGAACCTACCAAGCTGAGTACGGTAGGGGACG	717				
QY	661	GTAGAATTCGCGGTGTAGCAGTGAATTCGTAGAGATGCGGAGGAATACCGATGGCGAAG	720				
Db	718	AGGGAATTTCCGTTGGAGCGGTGAATGCAATTGAGATCGGAAAGAACACCAACGGCGAA	777				
QY	721	GCAGCCCCCTGGGATGACACTGACGCTCATGACGAAAGCGTGGGAGCAACAGCATTA	780				
Db	778	GCACTGTCTGGGCCGACACTGACCTGAGAGACGAAGCTAGGGAGCAATGGGATTA	837				
QY	781	GATACCCCTGG--TAGTCCAGCCCTAAAACGATGCTCAATTAGCTGTTGGGGTTTGAATCC	838				
Db	838	GAGACCCAGATAATCCATAGCCGTAACCGATGATACTAGGTGCTGTGCGACTCGACCC	897				
QY	839	TTG--GTAGCGTGTAAACGCGTGAATTTGAACCGCTCTGGGAGTACGGCCGCGAAGTTAA	896				
Db	898	GTGCACTGCTGTAGCTTAAACGCGTTAAGTATCCCGCTGGGAGTACGTTTCGCAAGATGA	957				

Qy	897	AACCTCAAAGGAATTGACGGGACCCGCAACAAGCGGTGGATGATGTGGATTAATTCGATGC	956						
Db	958	AACCTCAAAGGAATTGACGGGACCCGCAACAAGCGGTGGATGATGTGGATTAATTCGATGC	1017						
Qy	957	AACGCGAAAAACCTTACCTGCTTTCACATGTATACGGAACCTTGTGAGATATCTTGGTGC	1016						
Db	1018	AAAGCGAAGAACCTTACCGAGGCTTGACATGTCGCGGAATCTCTTGAAGAGAGGGGTGC	1077						
Qy	1017	CGAAAGGGAGCGGTAAACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1076						
Db	1078	CC--TCGGAAACCGGACACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1135						
Qy	1077	TGGTTAAAGTCCGCAACGAGCGCAACCTTGTTCATTAGTTGCCATCAATTAGTTGGCCA	1136						
Db	1136	TGGTTAAAGTCTCGCAACGAGCGCAACCTTGTTCATTAGTTGGCCA-CTATGAGTTGGAA	1194						
Qy	1137	CTCTAATGAGACTGCGGTGACAAACCGGAGGAAGTGGGATGACGTCAAGTCCTCATG	1196						
Db	1195	CCCTGAACAGACCGCGGTGTTAAGCCGAGGAAGAGAGGATGAGGCCAAGTCATCATG	1254						
Qy	1197	GCCTTTATGAGCAGGCTTTCACACGCTCATACATGCTCGGTACAGAGGCTCGCTAAGCCG	1256						
Db	1255	CCCTTTATGCTTGGGCGACACACGCTGTACATGCGCGGACAAAGGGTCTCGGATCTCG	1314						
Qy	1257	CGAGGTGTGCCAATCTCATAAACCGATCGTAGTCCGATCGCACTCTGCAACTCGAGT	1316						
Db	1315	CGAGGTGAGCTTAATCTCAAAACCGTCTCTAGTTCCGATTCGAGCTGCAACTGCTCT	1374						
Qy	1317	GGTGAAGTCGGAATCGCTAGTAATCCAGATCAG-CATGCTGCGGTGAATACGTTCCCG	1375						
Db	1375	GCATGAAGCAGGAATCGCTAGTAATCGCGGTGAGCATACGCGGTGAATCGTTCCCG	1434						
Qy	1376	GGCTTTGTACACACCGCCGTCACACCATGCGGAGTGAAGTTTACACAGAGTGGGTAGGCT	1435						
Db	1435	GGCTTTGTACACACCGCCGTCACACTATAGGAGTGGCCATGTTTGAAGTCAATTACCT	1494						
Qy	1436	AACC 1439							
Db	1495	TAAC 1498							

RESULT 3
LOCUS DU370470/c 793 bp DNA linear GSS 05-OCT-2005
DEFINITION 1098268193187 CHORI-243 Ovis aries genomic clone CH243-111G6,
genomic survey sequence.
ACCESSION DU370470
VERSION DU370470.1 GI:77100332
KEYWORDS GSS.
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 793)
AUTHORS Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and
Cockett,N.
TITLE Ovine BAC End Sequences from Library CHORI-243
JOURNAL Unpublished (2004)
COMMENT Other GSSs: 1098312102578
Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirknes@tigr.org
Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVI/JTC; http://www.jventerinstitute.org/).
Original Trace: 1098268193187 Trace 11: gnl|ti|91814376
Insert Length: 184000 Std Error: 0.00 row: G column: 6
Seq primer: S96
Class: BAC ends.
FEATURES
Location/Qualifiers
1..793
source


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|||||
241 GTGAGTAATGGCTCACCAGGCGACGATCCGTAATGGTCTGAGAGGATGATCAGTCAC 300
QY ACTGGGACTGAGACACGGCCAGACTCTTACGGGAGGCGACAGTGGGGAATTTGGACAA 364
Db ACTGGAACTGAGACACGGTCCAGACTCTTACGGGAGGCGACAGTGGGGAATATTTGACAA 360
QY TGGGGGCAACCTTGATCCAGCCATCGCCGCTGTCTGAAGAAGGCTTTCCGGTTGTAAAGG 424
Db TGGGCGAAAGCCTGATCCAGCCATCGCCGCTGTCTGAAGAAGGCTTTCCGATTGTAAAGC 420
QY ACTTTTGTGAGGAGGAAATCCCGCTGGTTAATACCCGGCGGGGATGACATGACATCCBGAAG 484
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QY GGGCTCAACCTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTGCCTGACAGGGGGTAG 664
Db GGGCTCAACCTGGGAACCTGCAAACTGGCAAGCTAGAGTATGTTAGAGGCTGGTGG 660
QY AATTCGCGGTGAGCAGTGAATGCGTAGAGATCGGAGGAATACCGATGCGCAAGCGAG 724
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QY CCCCTGGGATGACACTGACGCTCATGCACGAAAGCGTGGGAGCAAAACAGGATTAGATA 784
Db CCACCTGGACTGACTACTGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGGATTAGATA 780
QY CCTGTGTAGTCACGCCCTAAACGATGTCAATTAGCTGTGGGGTTTGAATCCTTGGTA 844
Db CCTGTGTAGTCACGCCCTAAACGATGTCAATTAGCTGTGGGGTTTGAATCCTTGTAGT 840
QY GCCTGAGTCAACGGTGAATTTGACCGCTCGGGAGTACGCCCAAGGTTTAAACTCAA 904
Db G-GAGCTAACGATTAAGTTGACCGCTCGGGAGTACGCCCGCCAGTTTAAAACTCAA 899
QY GGAATTGACGGGACCGCACAAAGCGGTGATGATGTGGATT 946
Db TGAATTGACGGGCGCCGACACAGCGGTGGAGCATGTGGTTT 941
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RESULT 5

BZ439740
LOCUS BONDUS4TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDUS4, 1084 bp DNA linear GSS 13-DEC-2002
DEFINITION genomic survey sequence.

ACCESSION BZ439740
VERSION BZ439740.1 GI:26695676
KEYWORDS GSS.

SOURCE Brassica oleracea
ORGANISM Brassica oleracea

REFERENCE 1 (bases 1 to 1084)
AUTHORS Avele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

TITLE Whole genome shotgun sequencing of Brassica oleracea and its
JOURNAL application to gene discovery and annotation in Arabidopsis
PUBMED Genome Res. 15 (4), 487-495 (2005)
15805490

COMMENT Other GSSs: BONDUS4TR
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523

FEATURES
source 1..1084
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 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
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 /clone_lib="BO_1.6_2_KB_tot"
 /notes="Vector: pHO51; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHO51 using BstXI linkers"

Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.
 Location/Qualifiers

ORIGIN

Query Match 42.8%; Score 615.8; DB 11; Length 1084;
Best Local Similarity 75.8%; Pred. No. 5.9e-178;
Matches 824; Conservative 1; Mismatches 234; Indels 28; Gaps 4;
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QY 622 GCATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGGGGTAGAAATCCGCGTGTAGCAG 681
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QY 682 TGAATGCGGTAGAGATGCGGAGGAATACCGATGGCGGAAGCGACCCCTCGGGATGACACT 741
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Db 463 GACACTGAGAGACGAAAGCTAGGGAGCGAATGGGATTAGATACCCCGAGTAGTCTTAGCC 522
QY 802 CTAAACGATGTCAATTTAGCTGTGGGGTTTGAATCCTTG--GTACGCTAGCTTAACGCGT 859
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QY 860 GAAATTTGACCGGCTGGGAGTACCGCGCAAGGTTAAAACTCAAAAGGAATTTGACGGGGAC 919
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DEFINITION genomic survey sequence.
ACCESSION BZ447500
VERSION BZ447500.1 GI:26712943
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 1053)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other_GSSs: BONKF40TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
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total DNA inserted into pHD1 using BstXI linkers"

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Query Match 42.6%; Score 613.8; DB 11; Length 1053;
Best Local Similarity 76.0%; Pred. No. 2.4e-177;
Matches 819; Conservative 1; Mismatches 229; Indels 28; Gaps 4;

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342 CACGAGTGGGGAATTTTGGACAATGGGGCAACCCCTGATCCAGCCATGCCCGGTGCTGA 401
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LOCUS BZ431523 1010 bp DNA linear GSS 13-DEC-2002
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 genomic survey sequence.
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 VERSION BZ431523.1 GI:26677909
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1010)
 Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
 Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
 Whole genome shotgun sequencing of Brassica oleracea and its
 application to gene discovery and annotation in Arabidopsis
 Genome Res. 15 (4), 487-495 (2005)
 15805490
 Other GSSs: BONHD88TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
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 DB |||||
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 890 GAATTTTCCGCAATGGGCGGAAACCTTGACGAGCAATGCGCGTGGAGGTAGAAGCCCTA 831
 QY 412 CGGGTTGTAAAGACTTTTGTACAGGAGGAATCCCGCTGGTTAATACCGCGGGGATG 471
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 QY 772 ACAGGATTAGATACCCCTGCTAGTCCACGCGCTAAACGATGTCAATTAGCTGTTGGGGGTT 831
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 QY 890 AGGTTAAACTCAAAAGGAATTGACGGGAGCCCGCACAAAGCGGTGGATGATGTGGAATTAAT 949
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 ASNC1602.b2 HF10_10-07-02 uncultured marine microorganism
 HF10_10-07-02 genomic clone HF0010_017B09, genomic survey sequence.
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 VERSION DU743187.1 GI:85753021
 KEYWORDS GSS.
 SOURCE uncultured marine microorganism HF10_10-07-02
 ORGANISM uncultured marine microorganism HF10_10-07-02
 unclassified sequences; environmental samples.
 REFERENCE 1 (bases 1 to 1033)
 AUTHORS DeLong E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,
 Prigard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
 and Karl,D.M.
 TITLE Comparative genomics reveals ecological trends in stratified
 microbial communities in the ocean's interior
 JOURNAL Science (2006) In press
 COMMENT Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
 Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson
 and Edward DeLong
 US DOE Joint Genome Institute
 US DOE Joint Genome Institute
 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
 Tel: 617-253-5271
 Fax: 617-253-2679
 Email: PMRichardson@lbl.gov; delong@mit.edu
 North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
 DNA library prepared from marine picoplankton in the less than 1.6

um, greater than 0.22 um fraction. Sample Date: 10/7/2002
Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C
Salinity 35.08 psu Oxygen: 204.6 umol/kg
Class: forssmid ends.

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QY	708	ACCGATGGCGAAGGAGCGCCCTCGGGATGAACCTGAACGCTCATGCAAGAAACGCTGGGGA	767	
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VERSION	BZ426201.1
KEYWORDS	GI:26667713
SOURCE	GSS.
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REFERENCE	Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Unterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
AUTHORS	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
TITLE	Genome Res. 15 (4), 487-495 (2005)
JOURNAL	15805490
PUBMED	Other GSSs: BONDZ28TR
COMMENT	Contact: Chris Town
	TIGR
	9712 Medical Center Drive, Rockville, MD 20850, USA

FEATURES
SOURCE

ORIGIN
Query
Best

Qy	282	GGTGTGAGAGGATGATCCGCCACACCTGGGACTGAGACACGGCCAGACTCTTACGGGAGG	341
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Qy	342	CAGCAGTGGGAAATTTGGCAATGGGGCAACCCCTGATCCAGCCATCGCGCTGTCTGA	401
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Qy	402	AGAAGGCCTTCGGGTGTGAAGGACTTTCTCAGGAGGAGAAATCCCGCTGTTAATACCC	461
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Qy	762	TGGGGAGCAAAACAGGATTAAGTATACCTCGTGTAGTCCAGCCCTAAACGATGTCAATTAGCT	821
Db	498	AGGGAGCGAATGGATTAATACCCAGTACTAGTCTTACCGTAAACGATGATAGGC	439
Qy	822	GTGGGGGTTTGAATCTCTTG-GTAGCGTAGCTAAACCGGTGAATTAACCGCTGGGAG	879
Db	438	GCTGTGCTATCGACCGCTGCAGTGTGTAGCTAACGCGTTAAGTATCCCGCTGGGGAG	379
Qy	880	TACGGCGGCNAGGTTAAACTCAAGGATTTGACGGGGACCCGCCAACAGGGTGGATGAT	939
Db	378	TACGTTGCGCAAGAAATGAAACTCAAGGAAATTTGACGGGGGCCGCCAACAGCGGTGGAGCAT	319
Qy	940	GTGGATTAATTCGATGCAACGCGGAAACCTTACCTGCTCTTACCATGTACGGAACCTGG	999
Db	318	GTGGTTTAATTCGATGCAAGCGAAGAACCTTACCGAGGGCTTGACATGCGCGAATCCTC	259
Qy	1000	TAGAGATATCTTGGTGCAGGAGGAGCGGTAAACAGAGTGTGCTGATGCTGTCTGCTAG	1059
Db	258	TTGAAAGAGAGGGGTGCC--TTCCGGAAACGCGGACACAGGTGTGCTGCTGCTAG	201
Qy	1060	CTGCTGCTGAGATGTTGGGTTAAGTCCCGGAAACGAGCGCAACCTTGTCTATTAGTTGC	1119
Db	200	CTGCTGCCGTAAAGTGTGTGGTTTAAAGTCCCGGAAACGAGCGCAACCTTGTCTATTAGTTGC	141
Qy	1120	CATCATTTAGTTGGGCACCTAATGAGACTGCGCGGTGACAAACCGGAGGAAGTGGGGAT	1179
Db	140	CACCGTTAGTTTGGAAACCTGACAGACTGCGCGGTGATTAAGCCGGAGGAGTGAAGAT	81
Qy	1180	GACGTCAAGTCTCATGGGCCCTTTATGACGAGGCGCTTACACGCTATACATATGCTGCTAC	1239
Db	80	GACGTCAAGTCTCATGGGCCCTTTATGACGAGGCGCTTACACGCTATACATATGCTGCTAC	21
Qy	1240	AGAGGGTCCGTAGCCGCGA	1259
Db	20	AAAGGGTCCGATCCCGCGA	1
RESULT 10			
CK280527			
LOCUS			
DEFINITION			
CK280527 889 bp mRNA linear EST 02-AUG-2004			
EST743249 Nicotiana benthamiana mixed tissue cdna library.			

normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5' end, mRNA sequence.

CK280527

CK280527.1 GI:39850196

EST.

Nicotiana benthamiana

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 889)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST743250

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/

Seq primer: ART TAG GTG ACA CTA TAG.

Location/Qualifiers

1. 889

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NBMA117"

/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"

/lab_host="DH108-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

Query Match 41.6%; Score 599.4; DB 5; Length 889;

Best Local Similarity 81.8%; Pred. No. 6.3e-173;

Matches 727; Conservative 1; Mismatches 158; Indels 3; Gaps 3;

Qy 7 GTTTGATCTGCTCAGATTGAACCTGGCGGCGATGCTTTACACATGCAAGTCGAACGGT 66

Db 1 GTTTGATCATGCTCAGATTGAACCTGGCGGCGGCGCTTAACACATGCAAGTCGAGCGG 60

Qy 67 AACA-GGGTGTCTGACC-GCTGACAGTGGCGGAACGGGTGAGTAAATGCTTCGGAATGTA 124

Db 61 AGCAGGGTACTTGTACCTGGTGGCGAGCGGCGGCTGAGTAAATGCTTAGGAATCTG 120

Qy 125 CCGTGTAAATGGGGGATAGTCTCGCGGAAACCGCGGATTAATACCGCATACGCCCTGAGGGG 184

Db 121 CCGTGTAGTGGGGGATTAACGCTCGGAAACGCGGCTTAATACCGCATACGCCCTGAGGAG 180

Qy 185 AAAGCGGGGATCGAAAGACCTCGGCTTATACGAGCGCGGCTGATGATTAGCTAGTTTG 244

Db 181 AAAGCAGGGGACCTTCGGGCGCTTCGCTATCAGATGAGCCTAGGTCGGAATTAGTATTG 240

Qy 245 GTGAGGTAAAGCTCACCAGGCGAGATCAGTAGCGGCTCTGAGAGGATGATCCGCCAC 304

Db 241 GTGAGGTAAAGCTCACCAGGCGAGATCAGTAGCGGCTCTGAGAGGATGATCAGTCAC 300

Qy 305 ACTGGACTGAGACACGGGCCAGATCTCTACGGGAGGACGACGTGGGGAAATTTTGACAA 364

RESULT 10

CK280527

LOCUS

DEFINITION

CK280527 889 bp mRNA linear EST 02-AUG-2004

EST743249 Nicotiana benthamiana mixed tissue cdna library.

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Db 301 ACTGGAACAGACACGGTCCAGACTCCTACGGGAGGAGCAGCAGTGGGAAATATGGACAA 360
Qy 365 TGGGGGCAACCTGATCOAGCCATGCGCGTGTCTGAAGAAGGCGCTTCGGGTGTAAAGG 424
Db 361 TGGGCGAAAGCCTGATCCAGCCATGCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGC 420
Qy 425 ACTTTTCTCAGGGAGGAAATCCCGCTGTTTAATACCCGCGGGATCAGACAGTACCBGAAG 484
Db 421 ACTTTAAAGTTGGGAGGAGGCGAGTTACCTAAATACGTGATGTTTTCACGTTACCGACAG 480
Qy 485 AATAAGCACCGGCTAACTAGCTGCGACAGCCGCGTAAATACGTAGGGTCAAGCGTTAA 544
Db 481 AATAAGCACCGGCTAACTCTGTGCGACAGCCGCGTAAATACAGAGGTGCAAGCGTTAA 540
Qy 545 TCGGAATTAATCGGCGTAAAGCGTGCAGAGCGGTTTTGCAAGTCTCATGTGAAAGCCCC 604
Db 541 TCGGAATTAATCGGCGTAAAGCGCGTAGTGGTTTTGTTAAAGTTGATGTGAAATCCCC 600
Qy 605 GGGCTCAACCTGGGAACGGCAATTGGAGACTGCGAGACTAGAGCTAGAGTCGTCAGAGGGGGTAG 664
Db 601 GGGCTCAACCTGGGAACCTGCATCCAAACTGGCAAGCTAGAGTATGTTAGAGGGTGGTGG 660
Qy 665 AATTCCGCGTGTACAGTGAATCCGTAGAGATCGGAGGAATACCGATGCGCGCAAGGCAG 724
Db 661 AATTTCCTGTGTAGCGGTGAATCGGTAGATATAGGAAGGAACACCAAGTGGCGAAGSGGA 720
Qy 725 CCCCCTGGGATGA CACTGACGCTCATGCA CGAAAGCGTGGGAGCAAAACAGGATTAGATA 784
Db 721 CCACCTGGACTGATCTGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGGATTAGATA 780
Qy 785 CCCTGGTGTAGTCCAGCCCTAAACGATGTCATTAAGCTGTTGGG-GGTTTGAATCCTTGGT 843
Db 781 CCCTGGTGTAGTCCAGCCGCTAAACGATGTCATTAAGCTGTTGGGAGCCCTTGAGCTCTTAGT 840
Qy 844 AGCGTAGCTAACCGCTGAAATTTGACCGCTCGGGGAGTACGGCCGCAAGG 892
Db 841 GGCGCAGCTAACGCTTAAGTTGACCGCTCGGGGAGTACGGCCGCAAGG 889

RESULT 11
LOCUS BH814966/c
DEFINITION pBPC15 Maize B chromosome PCR DNA library Zea mays genomic clone
ACCSSION BH814966
VERSION BH814966.1 GI:31249923
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1143)
Cheng, Y.M. and Lin, B.Y.
Cloning and characterization of maize B chromosome sequences
derived from microdissection
Genetics 164 (1), 299-310 (2003)
12750341
Contact: Bor-yaw Lin
Department of Molecular Biology
National Chung Hsing University
250 Kuo Kuang Rd, Taichung 402, Taiwan (ROC)
Tel: 886-4-2285-1885
Fax: 886-4-2287-4879
Email: bylin@dragon.nchu.edu.tw
Insert Length: 1143 Std Error: 0.00
Class: PCR fragment.
Location/Qualifiers
1..1143
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="L289"
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FEATURES
Source
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/clone="pBPC15"
/sex="hemaphrodite"
/cell_type="Pollen mother cells"
/dev_stage="Meiosis I"
/lab_host="DH5alpha"
/clone_lib="Maize B chromosome PCR DNA library"
/notes="Vector: pBSK-; The library was constructed from
microdissected B chromosome DNA."

ORIGIN
Query Match 41.6%; Score 599.4; DB 11; Length 1143;
Best Local Similarity 87.6%; Pred. No. 6.8e-173;
Matches 691; Conservative 0; Mismatches 91; Indels 7; Gaps 3;

Qy 652 CAGAGGGGGGTAGAAATTCGCGTGTAGCAGTGAATCCGTAGAGATCGCGAGGAATACCG 711
Db 1143 CAGAGGGGGGTAGAAATTCACGCTGTAGCAGTGAATCCGTATATATGTGGAGGAACCG 1084
Qy 712 ATGCGGAAGGCGACCCCTCGGATGACACTGACGCTCATGCAGAAAGCGTGGGAGCAA 771
Db 1083 ATGCGGAAGGCGACCCCTCGGTCAGATTGACGCTCATGCAGAAAGCGTGGGAGCAA 1024
Qy 772 ACAGGATTAGATACCTCGGTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTGGGGTT 831
Db 1023 ACAGGATTAGATACCTCGGTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTGGGGTT 964
Qy 832 TGAATCCTTGGTAGCTAGCTAAACGCTGAAATTTGACCGCTCGGGAGTACGGCCGCAAG 891
Db 963 AATTGACGTTGTAAACGAGCTAAACGCTGAAAGTAGACCGCTCGGGAGTACGGTCGCAAG 904
Qy 892 GTTAAAACTCAAAGGAATTGACCGGGACCCGCAACAGCGGTGATGTGGATTAAATTC 951
Db 903 ATTAAACTCAAAGGAATTGACCGGGACCCGCAACAGCGGTGATGTGGATTAAATTC 844
Qy 952 GATGCAACCGCAAAACCTTACCTGCTTTGACATGTA CGAACTTGGTAGAGATATCTT 1011
Db 843 GATGCAACCGCAAAACCTTACCTGCTTTGACATGTA CGAACTTGGTAGAGATATCTT 784
Qy 1012 GGTGCGGAAAGGAGCGGTAAACAGGTGCTGCATGGCTGCTGACGCTCGTCTGCTGA 1071
Db 783 AGTGCTCGAAAGAGAACCAAGTACACAGGTGCTGCATGGCTGCTGACGCTCGTCTGCTGA 724
Qy 1072 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTCAATTAGTTGCCATCATTTAGTT 1131
Db 723 GATGTT--GGTTAAGTCCCGCAACGAGCGCAACCTTGTCAATTAGTTGCTTACGA-----AA 670
Qy 1132 GGGCACTTAATGAGACTGCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAGTCC 1191
Db 669 GGGCACTTAATGAGACTGCGGTGACAAACCGGAGGAAGGTGGGGAT-ACGTCAAGTCC 611
Qy 1192 TCATGGCCCTTATGAGCAGGCTTCAACGCTCATACAAATCGTTCGGTACAGAGGTCGCTA 1251
Db 610 TCATGGCCCTTATGGGTAGGGCTTCAACGCTCATACAAATCGTTCAGTACAGAGCCGCCA 551
Qy 1252 AGCGCGAGGTGGTGCCAAATCTCATAAACCGATCGTAGTCCGGATCGCACTCTGCAACT 1311
Db 550 ACCGCGAGGGGAGCTTAATCGCAGAAAGTATCGTAGTCCGATGTAGTCTGCAACT 491
Qy 1312 CGAGTGCCTGAAGTCGGAATCGCTAGTAAATCGCAGATCAGCATGCTCGGTGAATAGTT 1371
Db 490 CGACTGCATGAAGTTGGAATCGCTAGTAAATCGCGGATCAGCATGCTCGCGGTGAATAGTT 431
Qy 1372 CCGGGTCTTGTAACACACCGCCGTCACACATGGGAGTGGTTTACACGAGAGTGGTA 1431
Db 430 CCGGGTCTTGTAACACACCGCCGTCACACATGGGAGTGGTTTACACGAGAGTGGTA 371
Qy 1432 GGCTAACCG 1440
Db 370 GCTTAACCG 362

RESULT 12
BH705272
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LOCUS	BH705272	1079 bp	DNA	linear	GSS 20-FEB-2002
DEFINITION	BOMKA47F BO_2_3_KB Brassica oleracea genomic clone BOMKA47, genomic survey sequence.				
ACCESSION	BH705272				
VERSION	BH705272.1				
KEYWORDS	GSS.				
SOURCE	Brassica oleracea				
ORGANISM	Brassica oleracea				
REFERENCE	1 (bases 1 to 1079) Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Uteerback,T.R., Wortman,J.R., White,O.R. and Town,C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)				
AUTHORS	1. (bases 1 to 1079) Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Uteerback,T.R., Wortman,J.R., White,O.R. and Town,C.D.				
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis				
JOURNAL	Genome Res. 15 (4), 487-495 (2005)				
PUBMED	15805490				
COMMENT	Other_GSSs: BOMKA47TR Contact: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF Class: sheared ends.				
FEATURES	Location/Qualifiers 1..1079 /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="TO1000DH3" /db_xref="taxon:3712" /clone="BOMKA47" /clone_lib="BO_2_3_KB" /notes="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"				
ORIGIN	Query Match 41.6%; Score 599; DB 11; Length 1079; Best Local Similarity 75.4%; Pred. No. 8.8e-173; Matches 795; Conservative 1; Mismatches 232; Indels 27; Gaps 3;				
QY	215	ACGAGCAGCGCGCTCTGATTAGCTAGTTGGTGAAGTAAAGGACTTTTGTTCAGGAGGAAATCCCGCTGGTT	274		
Db	50	AGGAGGGGCTCGGCTCTGATTAGCTAGTTGGTGAAGTAAAGGACTTTTGTTCAGGAGGAAATCCCGCTGGTT	109		
QY	275	AGTAGCGGCTTGAGAGGATGATCCGCCACACTGGGACTGAGACACGCGCCAGACTCCTA	334		
Db	110	AGTAGCTGTCGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCTA	169		
QY	335	CGGAGGCGACGAGTGGGAAATTTTGACATATGGGCAACCTTGATCCAGCCATGCCGG	394		
Db	170	CGGAGGCGACGAGTGGGAAATTTTCCGCAATGGGCGCAAGGCTGACGAGCAATGCCGG	229		
QY	395	TGTCCTGAAGAAGCCCTTCGGGTTGTAAAGGACTTTTGTTCAGGAGGAAATCCCGCTGGTT	454		
Db	230	TGGAGTAGAGGCTTACGGGCTCTGAACTCTTTTCCAGAGAGAA-----	277		
QY	455	AATACCCGGCGGGATGACAGTACCBGAAGAATAAGCACCGGCTAACTACGTGCCAGCAG	514		
Db	278	-----GCAATGACGCTATCTGGGGAATAAGCATCGGCTAACTCTGTGCCAGCAG	326		
QY	515	CCGCGGTAATACGTAGGTCGAAGGTTAATCGGAATTACTGGGCTGAAGCGTGGCAG	574		
Db	327	CCGCGGTAATACAGAGGATGCAAGGCTTATCCGGAATGATTTGGGCGTAAAGCGTCTGTAG	386		
QY	575	GCGGTTTTCAAGTCTGATGTCAAAGCCCGGCTCAACCTGGGAACGGCAATTCGAGACT	634		
Db	387	GTGGCTTTTTAAGTCGCGCTCAATCCAGGGCTCAACCTTGGACAGGCGGTGGAAC	446		
QY	635	GCAAGACTAGAGTGGCTCAGAGGGGGGTAGAAATTCGCGGTGTAGCAGTGAATTCGCTAGA	694		
Db	447	ACCAAGCTTTGAGTACGTTAGGGGCAGAGGGAATTTCCGGTTGGAGCGGTGAATTCGCTAGA	506		
QY	695	GATCGCGAGGAATACCGATGGCGAAGCAGCCCTCTGGGATGACACTGACGCTCATGCAC	754		
Db	507	GATCGGAAGAACAACAACGCGGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGAC	566		
QY	755	GAAAGCGTGGGAGCAAAACAGGATTAGATAACCTCTGGTAGTCCACGCGCTAAACGATGCA	814		
Db	567	GAAAGCTAGGGAGCGAATGGGATTAGATACCCCACTAGTCTTAGCCGTAACGATGGAT	626		
QY	815	ATTAGCTGTTGGGGTTTGAATCCTTG--GTAGCGTAGCTAACCGGTGAAATTCACGCGC	872		
Db	627	ACTAGCGCTGTGCGTATCGACCCGCTGCAGTGTGTAGCTTAACCGGTTAAGTATCCCGCC	686		
QY	873	TGGGAGTAGACGCCCAAGGTTAAACTCAAGGAATTGACGGGGACCCGCCACAACGGGT	932		
Db	687	TGGGAGTAGCTTTCGAAGAATGAACCTCCAAGGAATTGACGGGGGCCGCCACAACGGGT	746		
QY	933	GGATGATGTGGAATTAATTTCGATGCAACGCGGAAAAACCTTACCTGCTCTTGACATGTACGG	992		
Db	747	GGAGCATGTGTTTAATTTCGATGGCAAGCGAAGAACCTTACCAAGGCTTGACATGCCGC	806		
QY	993	AATCTGTTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACAACAGGTGCTGCATGGCTG	1052		
Db	807	AATCTCTTTGAAAGAGAGGGGTGCC--TTCCGGGAACGCGACACAGGTGGTGCATGGCTG	864		
QY	1053	TGCTCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACAGCGCAACCTTGTTCAT	1112		
Db	865	TGCTCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACAGCGCAACCTTGTTCAT	924		
QY	1113	TAGTTGCCATCATTTAGTTGGGCACCTCTAATGAGACTGCGGTGACAAACCGGAGGAAGG	1172		
Db	925	TAGTTGCCACCGTTCAGTTTGGAAACCCCTGACAGACTGCCCCGTGATACCGGAGGAGG	984		
QY	1173	TGGGATGACGTCAAGTCTCATGGCCCTTATGAGCAGGGCTTCAACGTCATACAAATGG	1232		
Db	985	TGAGGATGACGTCAAGTCTCATGGCCCTTATGAGCAGGGCTTCAACGTCATACAAATGG	1044		
QY	1233	TGCGTACAGAGGCTCGCTAAGCGCGGAGGTGGTGC	1267		
Db	1045	CCGGGACAAAGGCTCGCGATCCCGGAGGGTGAGC	1079		
RESULT 13	DU733613	976 bp	DNA	linear	GSS 27-JAN-2006
LOCUS	APK12330.g3 HF70_10-07-02 uncultured marine microorganism HF70_10-07-02 genomic clone HF0070_031B04, genomic survey sequence.				
DEFINITION	DU733613				
ACCESSION	DU733613				
VERSION	DU733613.1				
KEYWORDS	GSS				
SOURCE	uncultured marine microorganism HF70_10-07-02				
ORGANISM	uncultured marine microorganism HF70_10-07-02				
REFERENCE	1 (bases 1 to 976)				
AUTHORS	DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J., Prigard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W. and Karl,D.M.				
TITLE	Comparative genomics reveals ecological trends in stratified microbial communities in the ocean's interior				
JOURNAL	Science (2006) In press				
COMMENT	Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus, Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson and Edward DeLong US DOE Joint Genome Institute US DOE Joint Genome Institute 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA Tel: 617-253-5271 Fax: 617-253-2679 Email: PMRichardson@lbl.gov; delong@mit.edu Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/kg				

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			/db_xref="taxon:361144"
			/clone="HF0070_031B04"
			/cell_type="marine picoplankton, less than 1.8 um, greater than 0.22 um fraction"
			/clone_lib="HF70_10-07-02"
			/notes="Vector: pCtFOS; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 70 m depth on 10/7/2002, Coordinates: 22.45 N, 158 W Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/kg"
ORIGIN		Query Match 41.4%; Score 595.8; DB 14; Length 976;	
		Best Local Similarity 79.9%; Pred. No. 8.3e-172;	
		Matches 739; Conservative 0; Mismatches 182; Indels 4; Gaps 3;	
Qy	505	GTGCACGACGCGGTAATACGTAGGGTCAAGCGTTAATCGAATTACTGGCGGTAAA	564
Db	926	GGGCCACGACGCGGGGTATTACGGGGGGTACGAACTTATTGGAAATTCCTGGGGTAAA	867
Qy	565	GCGTGCCACGCGGTTTTCGAAGTCTCATGTGAAGCCCGGGCTCAACTGGGAACGGC	624
Db	866	CGGGGGTAGCGGTTTCGTTAAGTGGAGTGGAAGCCCGGGCTCACTGGGAACGCC	807
Qy	625	ATTGGAGACTGCAAGACTAGAGTCGTCAGAGGGGGGTAGAAATTCGCGTGTACGAGTGA	684
Db	806	TTCCAAACTGGCGAATAGAGTGTGTAGAGGGAAGTAGAATTTGATGTGACGGTGA	747
Qy	685	AAT- GCGTAGAGATGCGGAGGAATACCGATGGCGAAGCGAGCCCCCTGGGATGACACTGA	743
Db	746	AATGGCGTAGATATATCAAGGAATPACCAATGGCGAAGCGAGCTTCCTGGACTAACACTGA	687
Qy	744	CGCTCATGCAAGAGCGTGGGAGCAAAAGGATTAGATACCTCGTAGTCCACGCGCT	803
Db	686	CGCTAGAGTGGGAAGCGTGGGAGCAAAAGGATTAGATACCTCGTAGTCCACGCGCT	627
Qy	804	AAACGATGTCAATTAGCTGTGGGGTTTGAATCCCTTGGTAGCGTACTAACGCGTGA	863
Db	626	AAACGATGAGAACTAGCGGTTGGGAGGTTGCGCTCTTAGTGGCGCAGCTAACGCAATAAG	567
Qy	864	TTGACCGCTGGGAGTACGCGCCGACAGGTTTAAACTCAAGGAATTGACGGGACCCGC	923
Db	566	TTCTCCGCTGGGAGTACGCGCCGACAGGTTTAAACTCAATGAATTGACGGGGGCCCGC	507
Qy	924	ACAAAGCGTGATGATGTGGAATTAATTCGATGCAACGCAAAAACCTTACCTGCTTTGA	983
Db	506	ACAAAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGGAAGACCTTACCACCCCTTGA	447
Qy	984	CATGTA CGGAATCTGGTAGAGATATCTTGGTGCCGAAAGGACCGGTAAACAGGTGCT	1043
Db	446	CATACTCGGAATCTTTAGAGATAGATTGTTGTCCTTC- GGGAGCCGAGATACAGGTGCT	389
Qy	1044	GCATGGCTGTCGTGAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAAGCGCAAC	1103
Db	388	GCATGGCTGTCGTGAGCTCGTGTGAGATGTTGGGTAAAGTCCCGTAAGCGGCAAC	329
Qy	1104	CCTTGTCTATTAGTTGCCATC- ATTTAGTTGGGCACTCTTAATGAGACTGCCGTTGACAAAC	1162
Db	328	CCTTGTCTTATTGGCAGCATTCGTTGGTGGAACTCTAAGGAGACTGCCGTTGACAAAC	269
Qy	1163	CGGAGGAAGTGGGATGACGCTCAAGTCTCATGGCCCTTATGACGAGGCTTCAACGTT	1222
Db	268	CGGAGGAAGTGGGACGACGCTCAAGTCTCATGGCCCTTATGACGAGGCTTCAACGTT	209
Qy	1223	CATCAATGGTGGTACAGAGGGTGGCTTAAGCCCGGAGGTGGTGCCCAATCTCATAAACC	1282
Db		208	GCTACATGGGAGTACAAAGGGCGGCAAGCTAGCAATAGTAGAGCAATCCCAAAAGCT 149
Qy		1283	GATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCTAGTAATC 1342
Db		148	TCTCGTAGTCCGATTTGGGGTCTGCAACTCGACCCCATGAAGTCGGAATCGCTAGTAATC 89
Qy		1343	GCAGATCAGCATGCTCGGTTGATAGTTCCTCCGGGCTTTGTACACACCCGCGTCACACC 1402
Db		88	GCGAATCAAGATGTGCGGTTGATACGTTCCCGGGCTTTGTACACACCCGCGTCACACC 29
Qy		1403	ATCGGAGTGAAGTTTACCAAGAGTG 1427
Db		28	ATGGAAGTGAATGCACCAAGAGTG 4
RESULT 14		CK280528	884 bp mRNA linear EST 02-AUG-2004
LOCUS		EST743250	Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION			normalized, full-length Nicotiana benthamiana cDNA clone NEM117 5'
			end, mRNA sequence.
ACCESSION		CK280528	
VERSION		CK280528.1	GI:39850200
KEYWORDS		EST.	
SOURCE		Nicotiana benthamiana	
ORGANISM		Nicotiana benthamiana	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	
		asterids; lamids; Solanales; Solanaceae; Nicotiana.	
REFERENCE		1. (bases 1 to 884)	
AUTHORS		Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,	
		Staskawicz, B., Jin, H. and Baker, B.	
TITLE		Generation of EST sequences from Nicotiana benthamiana	
JOURNAL		Unpublished (2003)	
COMMENT		Other ESTs: EST743249	
		Contact: Robin Buell	
		The Institute for Genomic Research	
		9712 Medical Center Dr, Rockville, MD 20850, USA	
		Email: potato-array@tigr.org	
		Clones can be requested from the University of Arizona Genomics	
		Institute via http://genome.arizona.edu/orders/	
		Seq primer: CAG GAA ACA GCT ATG ACC.	
FEATURES		Location/Qualifiers	
source		1. .884	/organism="Nicotiana benthamiana"
			/mol_type="mRNA"
			/db_xref="taxon:4100"
			/clone="NEM117"
			/tissue_type="abiotic and biotic stress-treated leaves,
			callus tissue and root tissue"
			/lab_host="DHI08-Tona"
			/clone_lib="Nicotiana benthamiana mixed tissue cDNA
			library, normalized, full-length"
			/notes="Vector: pCMWsport6.1; Site 1: EcoRI; Site 2: NotI;
			supplier: RNA was isolated from Nicotiana benthamiana
			tissues that include callus, roots from liquid culture
			grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
			cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
			challenged leaves (Pseudomonas syringae pv tomato 12 hr;
			Xanthomonas campestris pv campestris 12 hr, 18hr;
			Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
			campestris pv vesicatoria 18hr). RNA was isolated from
			these tissues and pooled in approximately equal molar
			amounts."
ORIGIN		Query Match 41.2%; Score 592.8; DB 5; Length 884;	
		Best Local Similarity 81.6%; Pred. No. 6.8e-171;	
		Matches 721; Conservative 1; Mismatches 159; Indels 3; Gaps 3;	
Qy	7	GTTTGATCCTGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGGT 66	

Dd	1	GTTCATCATGGCTCAGATTGAACGCTGGCGGAGCGCTTAACACATGCAAGTCGAGCGGC	60
Qy	67	AACA-GGGTCTTGCCACC-GCTGACGAGTGGCGGAAACGGGTGAGTGAATGCGTCGGGAATGTA	124
Dd	61	AGCACGGGTACTTGTACTCTGGTGGCGAGCGCGGAGTGAATGCGTCGAGAACTCG	120
Qy	125	CGGTGAATCGGGGATAGCTCGGGGAGAAAGCCGGAATTAATACCGATACGCGCTTGAGGGGG	184
Dd	121	CCTGGTAGTGGGGGATAACGCTCGGAAACGGACGCTAATACCGCATACGTCCTACGGGAG	180
Qy	185	AAAGCGGGGATCGAAAGACCTCGCTTATACGAGCAGCGCGTCTGTGATTAGCTAGTTG	244
Dd	181	AAAGCAGGGACCTTCGGGCTTTCGCTATCAGATGAGCTAGTGGGATAGCTAGTTG	240
Qy	245	GTGAGGTAAAGAGCTCAACCAAGGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCGCCAC	304
Dd	241	GTGAGGTAAATGGCTCAACCAAGGCGAGATCCGTAACCTGCTCTGAGGAGTATCATGTAC	300
Qy	305	ACTGGGACTGAGACACGGCCGACAGCTCTACGGGAGCAGCATGTGGGGAATTTTGGACAA	364
Dd	301	ACTGGAACTGAGACACGGTCCAGACTCTACGGGAGCAGCATGTGGGGAATATTGGACAA	360
Qy	365	TGGGGCAACCTCATGATCCAGCCATGCGCGTGTCTGAAGAAGCCCTTCGGGTTGTAAGG	424
Dd	361	TGGCGAAAGCCCTGATCCAGCCATGCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGC	420
Qy	425	ACTTTTGTTCAGGGAGGAAATCCCGCTGGTTAATACCCGGCGGGATGACAGTACCCGAAAG	484
Dd	421	ACTTTAAGTTGGGAGGAGGAGTACCTAATACGTGATTGTTTGACGTTACCGACAG	480
Qy	485	AATAAGCACCGGCTAATCTAGTCCGAGCAGCCGCGTAAATACGTAGGGTGCAGCGTTAA	544
Dd	481	AATAAGCACCGGCTAATCTAGTCCGAGCAGCCGCGTAAATACAGAGGGTGCAGCGTTAA	540
Qy	545	TCGGAAATTAATCGGCGTAAAGCGTGGCGAGCGGTTTTCGAACTCTGATGTGAAGCCCC	604
Dd	541	TCGGAAATTAATCGGCGTAAAGCGGCGTGGTGGTTTGTAAAGTTGGATGTGAATATCCCC	600
Qy	605	GGGCTCAACCTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGGGGTAG	664
Dd	601	GGGCTCAACCTGGGAACCTGATCCAAATCTGGCAAGCTAGAGTATGGTAGAGGGTGGTG	660
Qy	665	AATTCGCGGTAGAGTGAATGCGTAGAGATGCGGAGGAATACCGATGGCGAAGCGAG	724
Dd	661	AATTTCTGTGTAGCGGTGAATGCGTAGATATAGGAAGGAACACACAGTGGCGAAGCGA	720
Qy	725	CCGCTGGGATGACATGACGCTCATGCACGAAGCGTGGGAGCAACAGGATTTAGATA	784
Dd	721	CCACCTGGAGTATGATCTGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGATTTAGATA	780
Qy	785	CCCTGGTAGTCCACGCGCTAAACGATGTCAATTAGCTGTGTGGG-GGTTTGAATCTCTTGT	843
Dd	781	CCCTGGTAGTCCACGCGGTAAACGATGTCAACTAGCGTTGGAGCCTTGAGCTCTTAGT	840
Qy	844	AGCGTAGCTAACCGCGTGAATTAACCGCTGGGAGTACGCGCG	887
Dd	841	GGCGAGCTAACCGCATTAAGTTGACCGCTGGGAGTACGCGCG	884
RESULT 15			
DU476609			
LOCUS			
DEFINITION			
109841575465 CHORI-243 Ovis aries genomic clone CH243-341M16,			
genomic survey sequence.			
ACCESSION			
DU476609			
VERSION			
DU476609.1 GI:77265954			
KEYWORDS			
GSS.			
SOURCE			
Ovis aries (sheep)			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;			
Fecora; Bovidae; Caprinae; Ovis.			
REFERENCE			
1 (bases 1 to 917)			

AUTHORS
TITLE
JOURNAL
COMMENT

Kirkness, E., Shetty, J., de Jong, P., McEwan, J. C., Oddy, H. and Cockett, N.
Ovine BAC End Sequences from Library CHORI-243
Unpublished (2004)
Other_GSSs: 1098421043133
Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirknes@tigr.org
Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVC); http://www.venterlinstitute.org/.
Original Trace: 1098415755465 Trace TT: gnl|ti|919020497
Insert Length: 184000 Std Error: 0.00 row: M column: 16
Seq primer: SP6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..917
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/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-341M16"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-243"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"

ORIGIN

Query Match	41.2%;	Score 592.8;	DB 14;	Length 917;
Best Local Similarity	80.9%;	Pred. No. 6.9e-171;		
Matches	717;	Conservative	1;	Mismatches 159; Indels 9; Gaps 2;
Qy	4	AGAGTTTGATCTCGGCTCAGATTGAACGCTGGCGGCATGCTTTTACACATGCAAGTCGAAC	63	
Dd	32	AGGTTTGATCTCGGCTCAGATTGAACGCTGGCGGCATGCTTTAAACATGCAAGTCGAAC	91	
Qy	64	GGTAAC-----AGGGTGTGTCACCGCTGACAGTGGCGAACCGGGTGAGTAATGCGT	115	
Dd	92	GGCAGCAGCACCTAAGCTTGTAGTGGCTGGCGAGTGGCGACCGGGTGAGTAACGCGT	151	
Qy	116	CGGAATGTACCTGTAAATGGGGATAGCTCGCGAAAGCCGGAATTAATACCGCATACGCC	175	
Dd	152	GGGAATCTGGCTCTAGAGGGGGATTAATCGGGGAAACTCGGGCTAATACCGCATATCT	211	
Qy	176	CTGAGGGGAAAGCGGGGATCGAAAGACCTCGCGTTATACGAGCAGCCGACGCTCTGATT	235	
Dd	212	CTAAGGAGAAAGCGGGGACCGAAAGGCTCGCGTGGGGATGAGCTGCGTCCGATT	271	
Qy	236	AGCTAGTTGGTAGGTAAGAGCTCACCAGGCGACGATCAGTAGCGGGTCTGAGAGATG	295	
Dd	272	AGCTAGTTGGTGGGTAAAGGGCTTACCAAGGCGATGATCGGTAGCTGGTCTGAGAGACG	331	
Qy	296	ATCCGCCACACTGGGACTGAGACACGGCCAGACTCTCTACGGAGGCGACAGTGGGGAAT	355	
Dd	332	ATCAGCCACACTGGGACTGAGACACGGCCAGACTCTCTACGGAGGCGACAGTGGGGAAT	391	
Qy	356	TTTGGACAATGGGGCAACCTGTATCCAGCCATGCGCGTGTCTGAAGAAAGCCTTCGGG	415	
Dd	392	ATTGGACAATGGGGCAACCTGTATCCAGCAATCGCGTGGGTGAAGAAGGCTTCGCGG	451	
Qy	416	TTGTAAGACATTTTGTCTAGGGAGGAATCCCGCTGGTTAATACCGCGGGGATGACAG	475	
Dd	452	TTGTAAGACCTTTTGTGGGGGAAAGAGCGATGTGTGAATAGCACATCGTGTGACGT	511	
Qy	476	TACCGAAGAAATAGCACCGGCTTAATCGTCCAGCAGCCGCGTAAATACGTAGGGTGC	535	
Dd	512	TACCTACAGAAAGACCGGCTTAATCTCGTCCAGCAGCCGCGTAAATACCGAGGTGC	571	
Qy	536	AAGCGTTAATCGGAATTAATCTGGGCGGTAAAGCGTGGCGAGCGGTTTTCGAAGTCTGATGT	595	

572	Db	 GAGCGTTAAATCGGAATTA	 CTGGCGCTAAAGGCGGTAGG	 CGCGTTTGGTAAGTTGGGTGT	631
596	Qy	GAAGCCCCGGCTCAACCT	GGGAACGCATTGGAGACT	GCAAAGACTGAGTGCCTCAGA	655
632	Db	GAAGCCCCGGGCTCAACCT	GGGAATGGCACTTGATCT	GCCTGGCTGAGTATGGTAGA	691
656	Qy	GGGGGTAGAAATTCGCGT	GTAGCAGTGAATTCGTAGAGAT	GCGGAGGAATACCGATGG	715
692	Db	GGGAGGCGGAATTCGCGT	GTAGCGTGAAATGCGTAGAT	ATCGGAAGCAACACCACTGG	751
716	Qy	CGAAGGCAGCCCCCTGGGAT	GNACACTGACGCTCATGCAC	GAAGCGTGGGGAGCAACAG	775
752	Db	CGAAGGCGGCTCTCTGGACCA	CTACTGACGCTGGGGT	CGAAAGCGTGGGAGCAACAG	811
776	Qy	GATTAGATACCTGGTAGT	GCACGCGCTAAACGATGT	CAATTAGCTGTTGGGGGTTTGAA	835
812	Db	GATTAGATACCTGGTAGT	GCACGCGCTTAACGATGAGNA	CTAGACGTTGGGAGGATAG	871
836	Qy	TCCTTT-GGTAGCGTAGCTAA	CGCGTGAAATTAACCGCCT	CTGGGAGT	880
872	Db	CTTTCACTGTTGCACTAA	CGCGTTAAGTTCTCCGCT	CTGGGAGT	917

Search completed: May 24, 2006, 02:54:40
Job time : 7453 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 22:12:15 ; Search time 980 Seconds
(without alignments)
10244.937 Million cell updates/sec

Title: US-10-678-023a-1

Perfect score: 1439.2

Sequence: 1 tggagagttgatcctggct.....agaagtggtaggtaacgcg 1440

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1439.2	100.0	1440	14	ADZ14078 Chromobac
2	1169.6	81.3	1610	10	ADB61691 16S rRNA
3	1165.8	81.0	1460	4	AAC86026 16S rDNA
4	1161.6	80.7	1532	2	AAQ26729 16S rRNA
5	1161.6	80.7	1532	10	ADB61686 16S rRNA
6	1160.6	80.6	1460	4	AAC86024 16S rRNA
7	1159.8	80.6	1488	10	ADB61690 16S rRNA
8	1159.8	80.5	1460	4	AAC86022 16S rRNA
9	1159	80.5	1544	10	ADB61693 16S rRNA
10	1159	80.5	110000	3	AAA81490_00
11	1159	80.5	110000	3	AAA81490_02
12	1159	80.5	110000	3	AAA81490_03
C 13	1159	80.5	110000	3	AAA81489_2
C 14	1159	80.5	110000	3	AAA81489_6
C 15	1159	80.5	110000	3	AAA81489_7
C 16	1159	80.5	172325	3	AAF21613
17	1159	80.5	349980	3	AAF21607
C 18	1159	80.5	349980	3	AAF21611

C	19	1159	80.5	349980	3	AAF21612	Aaf21612 Neisseria
	20	1159	80.5	349980	3	AAF21544	Aaf21544 Neisseria
	21	1157.6	80.4	1460	4	AAC86021	Aac86021 R. tenuis
	22	1152.6	80.1	1526	2	AAT01866	Aat01866 P. cepacia
	23	1152	80.0	1544	5	AAS11025	Aas11025 Neisseria
	24	1152	80.0	1544	10	ADB61692	ADB61692 16S rRNA
	25	1150	79.9	1459	4	AAC86028	Aac86028 16S rDNA
	26	1149.8	79.9	1478	4	AAC86023	Aac86023 R. purpur
	27	1149	79.8	1458	6	ABA02418	Aba02418 Type B am
	28	1149	79.8	1458	12	ADM32706	Adm32706 AOB Type
	29	1148.8	79.8	1532	2	AAQ64008	Aaq64008 16S rRNA
	30	1148.4	79.8	1426	4	AAC86029	Aac86029 16S rDNA
	31	1147.6	79.7	1464	10	ADB61688	ADB61688 16S rRNA
	32	1147.6	79.7	1485	4	AAC86030	Aac86030 16S rDNA
	33	1146.8	79.7	1535	2	AAV24295	Aav24295 Burkholde
	34	1146.8	79.7	1535	10	ADB61689	ADB61689 16S rRNA
	35	1145.8	79.6	1464	6	ABL40355	Ab140355 Sequence
	36	1145.8	79.6	1474	2	AAT18766	Aat18766 Pseudomon
	37	1145.6	79.6	1477	2	AAZ26285	Aaz26285 16S rDNA
	38	1137	79.0	1485	10	ADB61687	ADB61687 16S rRNA
	39	1135	78.9	1495	6	ABQ78660	Abq78660 Nucleotid
	40	1135	78.9	20844	3	AA81460	Aaa81460 N. mening
	41	1126.8	78.3	1496	12	ADQ16355	Adq16355 Nucleotid
	42	1126.8	78.3	1496	14	AEA01071	Aea01071 Bordetell
	43	1126	78.2	1530	14	ADM12666	Adm12666 Variovora
	44	1118.6	77.7	1451	4	AAF74542	Aaf74542 Burkholde
	45	1118.6	77.7	1451	10	ABX10819	Abx10819 Burkholde

ALIGNMENTS

RESULT 1

ADZ14078
ID ADZ14078 standard; DNA; 1440 BP.

AC ADZ14078;

XX
DT 16-JUN-2005 (first entry)

XX Chromobacterium suttsuga NRRL B-30655 16S ribosomal DNA.

DE Insecticide; pesticide; biological control agent; 16S ribosomal rNA;
KW 16S rRNA; cell culture; ds.

XX Chromobacterium suttsuga.

XX US2005074431-A1.

PN 07-APR-2005.

XX 01-OCT-2003; 2003US-00678023.

XX 01-OCT-2003; 2003US-00678023.

XX (MART/) MARTIN P A W.

PA (SHRO/) SHROPSHIRE A D S.

PA (GUND/) GUNDERSEN-RINDAL D E.

PA (BLAC/) BLACKBURN M B.

XX Martin PAW, Shropshire ADS, Gundersen-Rindal DE, Blackburn MB;

XX WPI: 2005-283752/29.

XX GENBANK; AY344056.

XX New biologically pure culture of a strain of Chromobacterium suttsuga sp.
PT nov. possessing insecticidal activity, useful for biocontrol of insect
pests.

XX Claim 3; SEQ ID NO 1; 19pp; English.

XX The present invention relates to a biologically pure culture of a strain
CC of Chromobacterium suttsuga sp. nov. The invention also relates to

```
CC insecticidally active metabolites obtained from the strain of
CC Chromobacterium suttsuga sp. nov. The invention is useful for biocontrol
CC of insect pests. The present sequence is the Chromobacterium suttsuga
CC NRRL B-30655 16S ribosomal DNA (rDNA).
XX
SQ Sequence 1440 BP; 359 A; 329 C; 460 G; 291 T; 0 U; 1 Other;

Query Match      100.0%; Score 1439.2; DB 14; Length 1440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGGAGGTTTGATCCTCGGCTCAGATTGAACCTCGCGCATGCTTTACACATGCAAGTCG 60
Db 1 TGGGAGGTTTGATCCTCGGCTCAGATTGAACCTCGCGCATGCTTTACACATGCAAGTCG 60
QY 61 AACGGTAACAGGGTGCTTTGCACCGCTGACGAGTGGCGAAGCGGGTGAATGCGTCGGAA 120
Db 61 AACGGTAACAGGGTGCTTTGCACCGCTGACGAGTGGCGAAGCGGGTGAATGCGTCGGAA 120
QY 121 TGTACCGTGTAAATGGGGATAGCTCGGCGAAGCGGGATTAATACCGCATACGCCCTGAG 180
Db 121 TGTACCGTGTAAATGGGGATAGCTCGGCGAAGCGGGATTAATACCGCATACGCCCTGAG 180
QY 181 GGGGAAACCGGGGATCCAAAGACCTCGCTTATACGAGCAGCGACGCTCTGATTAGCTA 240
Db 181 GGGGAAACCGGGGATCCAAAGACCTCGCTTATACGAGCAGCGACGCTCTGATTAGCTA 240
QY 241 GTTGTGAGGTAAAGAGCTCACCAGGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCG 300
Db 241 GTTGTGAGGTAAAGAGCTCACCAGGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCG 300
QY 301 CCACACTGGGACTGAGACACGGCCAGACTCTCTACGGAGGAGGAGCAGTGGGGAATTTTGG 360
Db 301 CCACACTGGGACTGAGACACGGCCAGACTCTCTACGGAGGAGGAGCAGTGGGGAATTTTGG 360
QY 361 ACNATGGGGCAACCTCATCCAGCCATGCCCGTCTGTAAGAGGCTTCGSGTCTGA 420
Db 361 ACNATGGGGCAACCTCATCCAGCCATGCCCGTCTGTAAGAGGCTTCGSGTCTGA 420
QY 421 AAGGACTTTTGTACGGAGGAGAAATCCCGCTGGTTAATACCCCGGGGGATGACAGTACCB 480
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QY 481 GAAGAAATGAACACCGGCTAACTAGTGCAGCAGCGCGGTAAATACGTAGGGTGCAGCG 540
Db 481 GAAGAAATGAACACCGGCTAACTAGTGCAGCAGCGCGGTAAATACGTAGGGTGCAGCG 540
QY 541 TTAATCGGAAATTACTGGGCGTAAAGCGTGCAGCGCGGTTTTCGAAGTCTGATGTAAAG 600
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QY 601 CCCCGGCTCAACCTTGGGAAACGGCAATGGAGACTGCAAGCTAGAGTGCCTCAGAGGGGG 660
Db 601 CCCCGGCTCAACCTTGGGAAACGGCAATGGAGACTGCAAGCTAGAGTGCCTCAGAGGGGG 660
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Db 721 GCAGCCCCCTGGGATGACACTGACGCTCATGCAAAAAGCGTGGGGAGCAAAACAGGATTA 780
QY 781 GATACCTGGTAGTCCAGCCCTAAACGATGTCATTAAGTCTGTCGGGGTTTGAATCCTT 840
Db 781 GATACCTGGTAGTCCAGCCCTAAACGATGTCATTAAGTCTGTCGGGGTTTGAATCCTT 840
QY 841 GGTAGGCTAGCTAAACGCTGAATTTGACCGCTGGGGATGACCGCGCAAGGTTTAAACT 900
Db 841 GGTAGGCTAGCTAAACGCTGAATTTGACCGCTGGGGATGACCGCGCAAGGTTTAAACT 900
QY 901 CAAAGGAATTGACGGGGACCCCGCACAAGCGGTGGATGATGTGGATTAATTCGATCAACG 960
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QY 961 CGAAAAACCTTACCTGCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTCCCGA 1020
Db 961 CGAAAAACCTTACCTGCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTCCCGA 1020
QY 1021 AAGGAGCCCTTAACACAGGTGCTGCATGGCTGCTGCAGCTCGTGTGCGTAGAGATGTTGGG 1080
Db 1021 AAGGAGCCCTTAACACAGGTGCTGCATGGCTGCTGCAGCTCGTGTGCGTAGAGATGTTGGG 1080
QY 1081 TTAAGTCCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCCATCATTTAGTTGGGCACTCT 1140
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QY 1141 AATGAGACTGCGGCTGACAAAACCGGAGGAAGTGGGATGACGTCAAAGTCTCTCATGSGCC 1200
Db 1141 AATGAGACTGCGGCTGACAAAACCGGAGGAAGTGGGATGACGTCAAAGTCTCTCATGSGCC 1200
QY 1201 TTATGACAGGGCTTCACAGTCAATCAATGGTCGTTACAGAGGTCGCTAAGCCGGAG 1260
Db 1201 TTATGACAGGGCTTCACAGTCAATCAATGGTCGTTACAGAGGTCGCTAAGCCGGAG 1260
QY 1261 GTGTGTCGAATCTCATAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGCCT 1320
Db 1261 GTGTGTCGAATCTCATAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGCCT 1320
QY 1321 GAAGTCGGAATCGGTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGCTCT 1380
Db 1321 GAAGTCGGAATCGGTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGCTCT 1380
QY 1381 TGTACACACCGCCGTCACACCATGGGAGTGAGTTTCACAGAAAGTGGTAGGCTAAACCG 1440
Db 1381 TGTACACACCGCCGTCACACCATGGGAGTGAGTTTCACAGAAAGTGGTAGGCTAAACCG 1440

RESULT 2
ADB61691
ID ADB61691 standard; DNA; 1610 BP.
XX
AC ADB61691;
XX
DT 04-DEC-2003 (first entry)
XX
DE 16S rRNA of Burkholderia pseudomallei DNA sequence.
XX
KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS Burkholderia pseudomallei.
XX
PN WO2003054162-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
PR 20-DEC-2001; 2001US-00029397.
XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
WPI; 2003-663255/62.
XX
Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
XX oligonucleotide.
```

Claim 4; Page 175; 208pp; English.

This invention relates to a novel method for isolating, depleting or separating a targeted nucleic acid, such as rRNA, from a sample comprising targeted and non-targeted nucleic acids. It effects a way of enriching for non-targeted nucleic acids such as mRNAs. Isolating sufficient quantities of high quality bacterial mRNA is a demanding process which impedes analysis of bacterial gene expression in the presence of host cells. A small percentage of bacterial mRNAs may be poly-A tailed, but these are targeted for degradation and tend to be unstable. As a result, the commonly employed method for mRNA purification with eukaryotic cells, oligo-dT capture, is ineffective. The present invention provides an alternative, more suitable method for mRNA purification from prokaryotes. The method of the invention comprises the incubation of a sample with a bridging oligonucleotide (containing a targeting region) and subsequently incubating with a capture oligonucleotide allowing the isolation of the target from the sample. The method is useful for depleting or isolating targeted nucleic acid, for example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may comprise any one of 64 fully defined sequences as given in the specification. The present sequence is that of a DNA sequence which represents the sequence of 16S rRNA of *Burkholderia pseudomallei* related to the invention.

SQ Sequence 1610 BP; 394 A; 383 C; 514 G; 319 T; 0 U; 0 Other;

Query Match 81.3%; Score 1169.6; DB 10; Length 1610;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1278; Conservative 1; Mismatches 156; Indels 5;

Qy	1	TGAGAGTTTGATCTCTGGCTCAGATTGAAACCTCGCGGCATGCTTTACATCATCGAAGTCG	60
Db	59	TGAGCAGTTTGATCTCTGGCTCAGATTGAAACCTCGCGGCATGCTTTACATCATCGAAGTCG	118
Qy	61	AACGCTAAACAGGCTGCTTGCCACCGCTGACGAGTGGCGAAACGGGTGAGTAAATGCGTCGAA	120
Db	119	AACGGCAGCACGGCTTCGGCTCGGCTGGTGGCGAGTCGCGAACGGGTGAGTTATACATCGGAG	178
Qy	121	TGTAACGTGTAAATGGGGGATAGCTCGGGGAAAGCCGGATTAATACCGCATACGCCCTGAG	180
Db	179	CATGTCCTGTAGTGGGGGATAGCCCGGCGAAAGCCGAATTAATACCGCATACGATCTGAG	238
Qy	181	GGGGAAGCGGGGATCGAAAGACCTCGCGTTATACGAGCAGCGCAGCTCTGATTAGCTTA	240
Db	239	GATGAAGCGGGGACCTTCGGGCTCGCGCTATAGGTTGGCCGATGCTGATTAGCTA	298
Qy	241	GTGTGTAGGTAAGAGCTTCAACGAGCGACGATCAGTAGCGGGTCTGAGAGATGATCCG	300
Db	299	GTGTGTGGGGTTAAGGGCCTTACGAGGCGACGATCAGTAGCTGTCTTGAGAGGACGACCG	358
Qy	301	CCACACTGGGACTGAGACACGGCCACAGACTCTTACGGGAGCGACAGTGGGGAAATTTTCG	360
Db	359	CCACACTGGGACTGAGACACGGCCACAGACTCTTACGGGAGCGACAGTGGGGAAATTTTCG	418
Qy	361	ACAAATGGGGGAAACCTGATTCAGGCATGCGCGCTGTCTGAAGAGGCTTTCGGGTGTGA	420
Db	419	ACAAATGGGGCGAAGCTGATTCAGCAATGCGCGCTGTGTGAAGAGGCTTTCGGGTGTGA	478
Qy	421	AAGGACTTTTGTTCAGGGAGGAAATCCCGCTGGTTTAATACCGCGGGGATGACAGTACCB	480
Db	479	AAGCACTTTTGTTCGGAAAGAAATCAATTCCTGGCTTAATACCGGAGTGGATGACGGTACC	538
Qy	481	GAAGAAATAAGCACCGGCTTAATCTACGTCCAGCAGCCCGGTAATACTGAGGGTGCAGGCG	540
Db	539	GAAGAAATAAGCACCGGCTTAATCTACGTCCAGCAGCCCGGTAATACTGAGGGTGCAGGCG	598
Qy	541	TTAAATCGGAATTAATCTGGCGTAAAGCGGTGCGCAGCGGCTTTGCAAGTCTGATGTCAAG	600
Db	599	TTAAATCGGATTAATCTGGCGGTAAGCGGTGCGCAGCGGCTTTGCTAAGACCGATGTGAAAT	658
Qy	601	CCCGCGGCTCAACCTGGGAAACGGCAATTGGAGACTGCAAGACTAGAGTGCGTCAAGCGGG	660

PD 28-JUN-2001.
XX
PF 28-DEC-2000; 2000WO-AU001611.
XX
PR 23-DEC-1999; 99AU-00004867.
XX
PA (CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.
XX
PI Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;
XX WPI; 2001-408656/43.
DR
XX Novel oligonucleotide probe or primer useful for detecting polyphosphate
PT accumulating organism in a sample, comprises a sequence that is unique to
PT 16S rDNA of polyphosphate accumulating organisms.
XX
PS Claim 4; Fig 3; 54pp; English.
XX
CC The sequences given in AAC86021-30 represent 16S rDNA sequences from
CC polyphosphate accumulating organisms (PAOs). Sequences which are unique
CC to these 16S rDNA sequences are used to create a probe or primer for
CC detecting the relevant organisms. The primer/probe sequences are useful
CC for detecting PAO cells in a sample, by treating cells in the sample to
CC fix cellular contents, contacting fixed cells with the primer/probe which
CC is labelled with a radiolabel, a reporter group or a hapten, under the
CC conditions which allow the probe to hybridize with 16S rDNA within the
CC fixed cell, removing unhybridized probe from the fixed cells, and
CC detecting the labeled probe-RNA hybrid by fluorescence in situ
CC hybridization. The primer/probe sequences are useful for identifying PAOs
CC that are capable of biologically removing phosphorus from waste water.
CC Rapid assessment of the presence of a number of PAOs in a waste water
CC sample, can be done using the primer/probe sequences. They allow quick
CC and convenient assessment of whether a sludge or waste water sample
CC includes PAOs and allows quantitation of PAO cells in samples. (Updated
CC on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 1460 BP; 359 A; 338 C; 475 G; 288 T; 0 U; 0 Other;

Query Match 81.0%; Score 1165.8; DB 4; Length 1460;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 1267; Conservative 1; Mismatches 149; Indels 2; Gaps 1;

QY 24 ATTGAAACCTGGCGCATGCTTACACATGCAAGTCGAACGCTACACGCTGCTTGCAAC 83
DB 1 ATTAACCGTGGCGCATGCTTACACATGCAAGTCGAACGCTACACGCTGCTTGCAAC 60
QY 84 GCTGACGAGTGGCGAAGCGGTGAGTAATGCGTCGGAATGTACCGTGTAAATGGGGATAGC 143
DB 61 GGTGGGAGTGGCGGAGCGGTGAGTAATGCGTACGGAACGTCGCTGAAGTGGGGATAAC 120
QY 144 TCGGCGAAGCCGGATTTAATACCGCATACGCCCTGAGGGGGAACGGGGGATCGAAAGA 203
DB 121 GCAGCGAAGCTACGCTAATACCGCATATTCTGTGAGCAGGAAAGCGGGGATCGCAAGA 180
QY 204 CTTCCGGTTATACGAGCAGCCACGCTGTGATTAGCTAGTTGGTAGGTTAAGAGCTCACCA 263
DB 181 CTTTCGCTTTGGGAGCGCCGATGTCGGATTAGCTAGTTGGTGGGTTAATGGCCATTCCA 240
QY 264 AGCGCACCATGATGACGGGCTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 323
DB 241 AGCGGACGATCCGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 300
QY 324 CCAGACTCTACGGGAGCAGGTGGGGAATTTGGACAATGGGGGACACCTGATCCA 383
DB 301 CCAGACTCTACGGGAGCAGGTGGGGAATTTGGACAATGGGGGAGGAGCTGATCCA 360
QY 384 GCCATGCCCGTGTCTGGAAGAAGGCTTCGGGTGTGAAAGGACTTTTGTACGGAGGAAA 443
DB 361 GCCATGCCCGTGTGAGGAAGAAGGCTTCGGGTGTGAAAGCTCTTTTCGGCGGGGAGAAA 420
QY 444 TCCCGCTGTTAATACCCCGCGGGGATGACAGTACCBGAAGAATAAGCACCGGCTAACTA 503
DB 421 TTGCTTGGGTTAATACCCCTGAGTAGATGACGGTACCCGAAATAAGAAGCACCGGCTAACTA 480

RESULT 4

AAQ26729

ID AAQ26729 standard; cDNA; 1532 BP.

XX AAQ26729;

XX AAQ26729;

DT 25-JAN-1993 (first entry)

QY 504 CGTCCAGACGCCCGCTAATCGTAGGTCGACGCGTTAATCGGAATTAATCGGCGCTAA 563
DB 481 CGTCCAGACGCCCGCTAATCGTAGGTCGACGCGTTAATCGGAATTAATCGGCGCTAA 540
QY 564 AGCGTGCAGAGCGGTTTTGCAAGTCTGATGTGAAAGCCCGGGCTCAACCTGGGAAACGG 623
DB 541 AGCGTGCAGAGCGGTTTTGTAAGTCAGATGTGAATCCCGGGCTCAACCTGGGAACTG 600
QY 624 CATTGGAGACTGCAAGACTAGAGTCGTCAGAGGGGGTGAATTCGCGGTGTAGCAGTG 683
DB 601 CATTGGAGACTGCAAGACTGAGGTTTGGCAGAGGGGGTGAATTCACGCTGTAGCAGTG 660
QY 684 AAATGCGTAGAGATGCCGAGGAAATACGATGGCGAAGCGACCCCTGGGATGACACTGA 743
DB 661 AAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGCGACCCCTGGGCAATACTAGA 720
QY 744 CGCTCATGCGAAGCGTGGGAGCAAAACAGGATTAAGATACCCCTGGTAGTCCACGCCCT 803
DB 721 CGCTCATGCGAAGCGTGGGAGCAAAACAGGATTAAGATACCCCTGGTAGTCCACGCCCT 780
QY 804 AAACGATGTCAATTAGTCTGTTGGGGTTTGAATCC--TTGGTAGCGTAGCTAAACGCGTGA 861
DB 781 AAACGATGTCAACTAGGTGTTGGGAGGTTAAAACCTTTTAGTGCCTAGCTAAACGCGTGA 840
QY 862 AATTGACCGCTGGGAGTAGCGCCGCAAGGTTAAACTCAAAGGAATTGACGGGACCC 921
DB 841 AGTTGACCGCTGGGAGTAGCGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGACCC 900
QY 922 GCACAAGCGGTGATGATGCGATTAAATTCGATCAACGCGAATAACCTTACCTGCTCTT 981
DB 901 GCACAAGCGGTGATGATGCGATTAAATTCGATCAACGCGAATAACCTTACCTGCTCTT 960
QY 982 GACATGACGGAACCTTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGTG 1041
DB 961 GACATGTCAGGAATCCTGGAGAGATTTGGGAGTGTCTGCAAGAGAACCTGAACACAGTG 1020
QY 1042 CTGCATGGCTGCTGCAGCTCGTCTGAGATGTGGGGTTAAGTCCCGCAACGAGCGCA 1101
DB 1021 CTGCATGGCTGCTGCAGCTCGTCTGAGATGTGGGGTTAAGTCCCGCAACGAGCGCA 1080
QY 1102 ACCCTTGTCAATTAGTTGCGCATCATTTAGTTGGGCACTCTAATGAGACTGCCGGTGACAAA 1161
DB 1081 ACCCTTGTCAATTAGTTGCGCATCATTTAGTTGGGCACTCTAATGAGACTGCCGGTGACAAA 1140
QY 1162 CCGGAGGAAGTGGGATGACGTCAAGTCTCATGGGCCCTTATGAGCAGGCGTTCACACG 1221
DB 1141 CCGGAGGAAGTGGGATGACGTCAAGTCTCATGGGCCCTTATGGGTAGGCGTTCACACG 1200
QY 1222 TCATACATGTCGCTACAGAGGTCGCTAAGCCGCGAGGTGGTGCCCAATCTCATAAAAAC 1281
DB 1201 TCATACATGTCGCTACAGAGGTTGCCAACCCGAGGGGGAGGCCAATCTCAGAAAGC 1260
QY 1282 CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTCGTCGTAAGTCGGAATCGCTAGTAAT 1341
DB 1261 CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTCGTCGTAAGTCGGAATCGCTAGTAAT 1320
QY 1342 CGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGCTTTGTACACACCGCCCGCTCACAC 1401
DB 1321 CGCGGATCAGCATGCGCGGTGAATACGTTCCCGGCTTTGTACACACCGCCCGCTCACAC 1380
QY 1402 CATGGGAGTGAGTTTCCACGAGAGTGGGTAGGCTTAACCG 1440
DB 1381 CATGGGAGCGGGTCTGCGCAGAGTAGTTAGCCTTAACCG 1419

XX 16S rRNA gene from Bordetella bronchiseptica.
DE rapid; examine; samples; test; identify; detect; ss.
XX Bordetella bronchiseptica.
XX JP04179480-A.
XX 26-JUN-1992.
XX 09-NOV-1990; 90JP-00304758.
XX 09-NOV-1990; 90JP-00304758.
XX (ZENK-) ZENKOKU NOGYO KYODO KUMIAI REN.
XX (NISE-) NIPPON SEIHUN KK.
XX WPI; 1992-263661/32.
XX 16-Sr-RNA gene of Bordetella bronchiseptica - DNA fragment for probe and
PT the detection of the gene using them allowing examination of many samples
PT in short period.
XX Claim 1; Page 1; l1pp; English.
XX This sequence represents the 16S rRNA gene from Bordetella
CC bronchiseptica. The 16S rRNA gene fragment was amplified by PCR and
CC isolated. The B. bronchiseptica 16S rRNA full-length gene was cloned and
CC the base sequence was determined. See also AA026730-6
XX
SQ Sequence 1532 BP; 378 A; 363 C; 490 G; 301 T; 0 U; 0 Other;

Query Match 80.7%; Score 1161.6; DB 2; Length 1532;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 1273; Conservative 1; Mismatches 161; Indels 5; Gaps 1;

QY 1 TGGAGAGTTTGATCCTGGCTCAGATTGAACCGCTGGCGCATGCTTTTACACATGCAAGTCG 60
DB 6 TGAAGAGTTTGATCCTGGCTCAGATTGAACCGCTGGCGCATGCTTTTACACATGCAAGTCG 65
QY 61 AACGGTAACAGGGTGTTCACCCGCTGACGATGCGGAAACGGGTGAGTAATGCTCGGAA 120
DB 66 GACGGCAGCAGCGGCTCGGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 125
QY 121 TGTACCGTGTAAATGGGGATAGCTCGCGAAGCGGATTAATACCCATACGCCCTGAG 180
DB 126 CGTCCCAAGTAGCGGGGGATTAATACCGAAGCGTGGCTAATACCGCATACGCCCTACG 185
QY 181 GGGGAAAGCGGGGATCGAAGACCTCGCGTTATACGAGCAGCGACGCTCTGATTAGCTA 240
DB 186 GGGGAAAGCGGGGACCTTCGGGCTCGCACTATTGGAGCGGCCGATATCGGATTAGCTA 245
QY 241 GTTGGTGAAGTAAAGCTACCAAGGCGAGATCAGTAGCGGGTCTGAGAGGATGATCCG 300
DB 246 GTTGGTGGGTAACGGGCTACCAAGGCGAGATCAGTAGCTGGTGGTGGTGGTGGTGGTGG 305
QY 301 CCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGCGCAGTGGGGAATTTGG 360
DB 306 CCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGCGCAGTGGGGAATTTGG 365
QY 361 ACAATGGGGCAACCTTGATCCAGCCATGCGCGTGTCTGAAGAAAGGCGCTTCGGGTTGTA 420
DB 366 ACAATGGGGCAACCTTGATCCAGCCATGCGCGTGTGCGATGAAGGCGCTTCGGGTTGTA 425
QY 421 AAGACATTTTGTAGGAGGAAATCCCGTGTGTTAATACCCGGCGGGGATGACAGTACCB 480
DB 426 AAGCACTTTTGGCAGGAAAGAAACGGCAGCGGCTAATATCTGTGCAACTGACGGTACCT 485
QY 481 GAAGAATAAGCACCAGGCTAATCTAGTGCAGCAGCGCGGTAAATACCTAGGGTGCAAGCG 540
DB 486 GCAGATAAGCACCAGGCTAATCTAGTGCAGCAGCGCGGTAAATACCTAGGGTGCAAGCG 545

QY 541 TTAATCGGAATTACTGGCGTAAAGCGTGCAGCGGTTTTGCAAGCTCTGATGTGAAG 600
DB 546 TTAATCGGAATTACTGGCGTAAAGCGTGCAGCGGTTTCGGAAGAAAGATGTGAAT 605
QY 601 CCCGGGCTCAACTGGGAAACGGCATTTGGAGACTGCAAGAAGCTAGAGTGCCTCAGAGGGG 660
DB 606 CCCAGGGCTTAAACCTTGGAACTGCATTTTAACTACCGGGCTAGAGTGTGTCTCAGAGGGAG 665
QY 661 GTAGAATTCCGCGTGTAGCAGTGAATGCGTAGAGATGCCGAGGAATACCGATGCCGAAG 720
DB 666 GTGGAATTCGCGTGTAGCAGTGAATGCGTAGATATGCCGAGGAACACCGATGCCGAAG 725
QY 721 GCAGCCCTCTGGGATGACACTGACCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTA 780
DB 726 GCAGCCCTCTGGGATGACACTGACCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTA 785
QY 781 GATACCTCTGTAGTCCACGCCCTTAAACGATGTCAATTAGCTGTGGGGTGTGAATCCTT 840
DB 786 GATACCTCTGTAGTCCACGCCCTTAAACGATGTCAATTAGCTGTGGGGCTTTCGGGCTT 845
QY 841 GGTAGCGTAGCTAACCGCGTGAATTTGACCGCTGGGAGTACCGCCGCAAGGTTTAAACT 900
DB 846 GGTAGCGTAGCTAACCGCGTGAATTTGACCGCTGGGAGTACCGTCCGCAAGATTTAAACT 905
QY 901 CAAAGGAATTGACGGGACCCGACAGCGGTGATGATGTGATTAATTCGATGCAACG 960
DB 906 CAAAGGAATTGACGGGACCCGACAGCGGTGATGATGTGATTAATTCGATGCAACG 965
QY 961 CGAAAAACCTTACCTGCTTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGCAGGA 1020
DB 966 CGAAAAACCTTACCTGCTTTGACATGTCTGTGAATCCGGAAGAGATTTGGAGTGTCTCGC 1025
QY 1021 AAGGAGCGCTTAACACAGGTGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1026 AAGGAGCGCTTAACACAGGTGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
QY 1081 TTAAGTCCCGCAACGAGCGCAACCTTGTCTATTAGTTGCCATCATTTTAGTTGGGCACTCT 1140
DB 1086 TTAAGTCCCGCAACGAGCGCAACCTTGTCTATTAGTTGCTACGAAA-----GGGCACTCT 1140
QY 1141 AATGAGACTCCCGGTGACAAAACCGGAGGAAGGTGGGATGACGTCAAAGTCTCATGGGCC 1200
DB 1141 AATGAGACTCCCGGTGACAAAACCGGAGGAAGGTGGGATGACGTCAAAGTCTCATGGGCC 1200
QY 1201 TTAATGACAGGGCTTACACAGTGCATACAATGCTGCTACAGAGGGTGCCTAAGCCGCGAG 1260
DB 1201 TTAATGAGTGGGCTTACACAGTGCATACAATGCTGCTGCGGACAGAGGTGCCTAAGCCGCGAG 1260
QY 1261 GTGCTGCAATCTCATAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGT 1320
DB 1261 GGGGAGCCATCCAGAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGT 1320
QY 1321 GAAGTGGGAATCGCTAGTAATTCAGATCAGATAGCTGCGGTGAATACGTTCCCGGGTCT 1380
DB 1321 GAAGTGGGAATCGCTAGTAATTCAGATCAGATAGCTGCGGTGAATACGTTCCCGGGTCT 1380
QY 1381 TGTACACACCGCCGCTCACACCATGGAGTGGTTCACAGAGTGGGTGAGCTAAGCTAACCG 1440
DB 1381 TGTACACACCGCCGCTCACACCATGGAGTGGTTCACAGAGTGGGTGAGCTAAGCTAACCG 1440

RESULT 5
ADB61686
ID ADB61686 standard; DNA; 1532 BP.
XX ADB61686;
AC ADB61686;
DT 04-DEC-2003 (first entry)
XX
DE 16S rRNA of Bordetella bronchiseptica DNA sequence.
XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;

Db 1321 GAAAGTCGGAATCGTAGTAATCGCGGATCGACATGTCGCGGTGAATACGTTCCCGGTCT 1380
Qy 1381 TGTCACACCCCGCGTCACACCATGGGAGTGAGTTTACCAAGAGTGGTAGGTAACCG 1440
Db 1381 TGTCACACCCCGCGTCACACCATGGGAGTGGGTTTACCAAGAGTAGTAGTACCGTAACCG 1440

RESULT 6

AAC86024
ID AAC86024 standard; cDNA; 1460 BP.

XX AC AAC86024;

XX 29-AUG-2001 (first entry)

XX DE R.tenuis 16s rDNA #3.

XX 16S rDNA; polyphosphate accumulating organism; PAO; probe; primer;
KW detection; phosphorus; waste water; sludge; ss.

XX OS Rhodocyclus tenuis.

XX XX WO200146459-A1.

XX XX 28-JUN-2001.

XX XX 28-DEC-2000; 2000WO-AU001611.

XX PR 23-DEC-1999; 99AU-00004867.

XX PA (CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.

XX PI Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;

XX DR WPI; 2001-408656/43.

XX Novel oligonucleotide probe or primer useful for detecting polyphosphate
PT accumulating organism in a sample, comprises a sequence that is unique to
PT 16S rDNA of polyphosphate accumulating organisms.

XX Claim 4; Fig 3; 54pp; English.

XX The sequences given in AAC86021-30 represent 16S rDNA sequences from
CC polyphosphate accumulating organisms (PAOs). Sequences which are unique
CC to these 16S rDNA sequences are used to create a probe or primer for
CC detecting the relevant organisms. The primer/probe sequences are useful
CC for detecting PAO cells in a sample, by treating cells in the sample to
CC fix cellular contents, contacting fixed cells with the primer/probe which
CC is labelled with a radiolabel, a reporter group or a hapten, under
CC conditions which allow the probe to hybridize with 16S rRNA within the
CC fixed cell, removing unhybridized probe from the fixed cells, and
CC detecting the labeled probe-RNA hybrid by fluorescence in situ
CC hybridization. The primer/probe sequences are useful for identifying PAOs
CC that are capable of biologically removing phosphorus from waste water.
CC Rapid assessment of the presence of a number of PAOs in a waste water
CC sample, can be done using the primer/ probe sequences. They allow quick
CC and convenient assessment of whether a sludge or waste water sample
CC includes PAOs and allows quantitation of PAO cells in samples

XX SQ Sequence 1460 BP; 366 A; 338 C; 471 G; 283 T; 0 U; 2 Other;

Query Match 80.6%; Score 1160.6; DB 4; Length 1460;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 1263; Conservative 1; Mismatches 153; Indels 2; Gaps 1;

Qy 24 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACCGTTAACAGGGTGCTTGCAAC 83

Db 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACCGTCAGCGACGCGGAGCAATCCT 60

Qy 84 GCTGACGAGTGGCGAACGGGTGAGTAATGCGTCGGAATGTACCGTGTAAATGGGGGATGC 143

Db 61 GGTGGCGAGTGGCGAACGGGTGAGTAATGCAATCGGAACGCTGCCCCCTGAAGTGGGGGATAAC 120

Qy 144 TCGGCGAAAGCCGATTAAATACCGCATACGCCCTGAGGGGGAAGACGGGGGATCGAAAGA 203
Db 121 GTAGCGAAGATTACGCTAATACCGCATATTCTGTGAGCAGGAAGACGAGGGGATCGCAAGA 180
Qy 204 CTTGCGGTTATA CGAGCAGCGCAGCTCTGATTAGCTAGTTGGTGAGTAAGAGCTCACCA 263
Db 181 CTTGCGCTTTGGGAGCGGCCGATTCGGATTAGCTAGTTGGTGGGGTAAAGGCTTACCA 240
Qy 264 AGGGACGATCAGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 323
Db 241 AGGCCACGATCCGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 300
Qy 324 CCAGACTCTTACGGGAGCGCAGCAGTGGGGAATTTGGACAAATGGGGGCAACCCCTGATCCA 383
Db 301 CCAGACTCTTACGGGAGCGCAGCAGTGGGGAATTTGGACAAATGGGCGAAGCCCTGATCCA 360
Qy 384 GCATGCCGCTGTCTGAAGAAGCCCTTCGGGTTGTAAGAGACTTTTGTGACGGAGGAAA 443
Db 361 GCCATGCCGCTGAGTGAAGAAGCCCTTCGGGTTGTAAGAGCTCTTTCGGGGGGAAGAAA 420
Qy 444 TCCGCTGGTTAATACCGCGGGGGATGACAGTACCBGAGAGATAAGCACCGGCTAACTA 503
Db 421 TTGCTCAGGATAATACCCCTGAGTAGATGACGGTACCCGAAAGAAAGACACCGGCTAACTA 480
Qy 504 CGTGCCACGAGCGCGGTAAATACGTAGGGTGCAGCGTTAATCGGAATTACTGGCGCGTAA 563
Db 481 CGTGCCACGAGCGCGGTAAATACGTAGGGTGCAGCGTTAATCGGAATTACTGGCGCGTAA 540
Qy 564 AGCGTGGCAGCGCGTTTTCAAAGTCTGATGTGAAGCCCGGGCTCAACTGCGGAACGG 623
Db 541 AGCGTGGCAGCGCGTTTGTGAAGACAGACGTCGAATCCCGGGCTCAACTGCGGAACGTG 600
Qy 624 CATTTGAGACTGCAGACTAGAGTGCCTCAGAGGGGGTGAATTCGCGCTGTAGCAGTG 683
Db 601 CGTTTGTGACTGCACGACTAGAGTGTGGCAGAGGGGGTGGAAATTCACGCTGTAGCAGTG 660
Qy 684 AAATGCGTAGAGATGCGGAGGAATACCGATGGCGAAGCAGCCCCCTGGGATGACACTGA 743
Db 661 AAATGCGTAGAGATGCGGAGGAACACCGATGGCGAAGCAGCCCCCTGGGCAATACTGA 720
Qy 744 CGCTCATGCAAGAAAGCGTGGGAGCAAA CAGGATTAGATACCTGTGTAGTCCACGCCCT 803
Db 721 CGCTCATGCAAGAAAGCGTGGGAGCAAA CAGGATTAGATACCTGTGTAGTCCACGCCCT 780
Qy 804 AAACGATGTCGAATAGCTGTTG--GGGTTTGAATCCTTGGTAGCTAGCTAGCGCTGA 861
Db 781 AAACGATGTCGAATAGCTGTTGTTGGGGTTAAACCCATTAGTCCGCTAGCTAACCGCTGA 840
Qy 862 AATTGACCGCTCGGGAGTAGTACGCCCGCAAGGTTAAAACTCAAAGGAATTCGACGGGACCC 921
Db 841 AGTTGACCGCTCGGGAGTAGTACGCCCGCAAGGTTAAAACTCAAAGGAATTCGACGGGACCC 900
Qy 922 GCACAAAGCGTGGATGATGGAATTAATTCGATGCACGCAAGAAAACCTTACCTGCTCTT 981
Db 901 GCACAAAGCGTGGATGATGGAATTAATTCGATGCACGCAAGAAAACCTTACCTGCTCTT 960
Qy 982 GACATGTACGGAACCTTGGTAGAGATATCTTGGTGGCCGAAAGGGAGCGCTTAACACAGTG 1041
Db 961 GACATGTACGGAACCTTGGTAGAGATATCTTGGGAGTTCGGGAGTGCCTGAACACAGGTG 1020
Qy 1042 CTGCATGGCTGTCGTCAAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGGGCA 1101
Db 1021 CTGCATGGCTGTCGTCAAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGGGCA 1080
Qy 1102 ACCCTTGTCTAATTAGTTGCCATCAATTTAGTTGGGCACTCTAATGAGACTGCGCGGTGACAA 1161
Db 1081 ACCCTTGTCTAATTTAGTTGCCATCAATTTAGTTGGGCACTCTAATGAAACTGCGCGGTGACAA 1140
Qy 1162 CCGGAGGAGGTGGGATGACGTCAAGTCTCATGCGCCCTTATGAGCAGCGGCTTCACAG 1221
Db 1141 CCGGAGGAGGTGGGATGACGTCAAGTCTCATGCGCCCTTATGGGTAGGGGCTTCACAG 1200

QY 1222 TCATACAAATGTCGTACAGAGGTGCTAAGCCGCGAGGTGGTGCCTAATCTCATAAAC 1281
DB 1201 TCATACAAATGTCGTACAGAGGTGCTAAGCCGCGAGGTGGTGCCTAATCTCATAAAC 1260
QY 1282 CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCTAGTAAT 1341
DB 1261 CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCTAGTAAT 1320
QY 1342 GCGAGATCAGATGCTGGGGTGAATACTGTCGGGGTCTTGTACACACCGCCCTCACAC 1401
DB 1321 GCGGATCAGATGTCGGGGTGAATACTGTCGGGGTCTTGTACACACCGCCCTCACAC 1380
QY 1402 CATGGAGTGAAGTTTACCCAGAGTGGGTGAGCTAAACCG 1440
DB 1381 CATGGAGTGAAGTTTACCCAGAGTGGGTGAGCTAAACCG 1419

RESULT 7
ADB61690
ID ADB61690 standard; DNA; 1488 BP.
XX
AC ADB61690;
DT 04-DEC-2003 (first entry)
XX
DE 16S rRNA of Burkholderia mallei DNA sequence.

XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.

XX Burkholderia mallei.

XX WO2003054162-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-US041014.

XX 20-DEC-2001; 2001US-00029397.

XX (AMBI-) AMBION INC.

XX Murphy GL, Whitley JP;

XX WPI; 2003-663255/62.

XX Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
PT oligonucleotide.

XX Claim 4; Page 174; 208pp; English.

XX This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for

CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Burkholderia mallei related to the
CC invention.

XX Sequence 1488 BP; 373 A; 344 C; 480 G; 291 T; 0 U; 0 Other;

QY Query Match 80.68; Score 1159.8; DB 10; Length 1488;
DB Best Local Similarity 89.14; Pred. No. 0;
Matches 1264; Conservative 1; Mismatches 149; Indels 5; Gaps 1;

QY 22 AGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGGTAACAGGGTCTTGCA 81
DB 1 AGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGGTACACGGGCTTCGGC 60
QY 82 CCGCTGACGAGTGGCGAACCGGTGAGTAATTCGCTCGGAATGTACCGTGTATGGGGGATA 141
DB 61 CTGGTGGCGAGTGGTGAACGGGTGAGTAATACATCGGAACATGTCTGTGTAGTGGGGATA 120
QY 142 GCTCGGGAAGCCGGATTAAATACCGCATACGCTTACCGATGAAAGCGGGGATCGAAA 201
DB 121 GCCCGGGAAGCCGGATTAAATACCGCATACGATCTGAGGATGAAAGCGGGGACCTTCG 180
QY 202 GACCTCGCTTATACGAGCAGCCGACGCTCTGATTAGCTAGTTGGTGAAGTAAAGCTCAC 261
DB 181 GGCCTCGCGCTATAGGTTGGCGATGGCTGATTAGCTAGTTGGTGGGTAAAGCCTAC 240
QY 262 CAAGCGCAGCATAGTAGCGGCTCTGAGAGATGATCGGCACACCTGGGACTGAGACAG 321
DB 241 CAAGCGCAGCATAGTAGCTGCTGAGAGACGACCAACGACCACTGGGACTGAGACAG 300
QY 322 GCCCAGACTCTACGGGAGCAGCAGTGGGGAATTTTGGCAATGGGGGCAACCTGATC 381
DB 301 GCCCAGACTCTACGGGAGCAGCAGTGGGGAATTTTGGCAATGGGGGCAACCTGATC 360
QY 382 CAGCCATGCGCGCTGCTGAAAGAGGCTTTCGGGTGTGTAAGGACTTTTGTTCAGGAGGA 441
DB 361 CAGCAATGCCCGCTGTGTGAAGAGGCTTTCGGGTGTGTAAGGACTTTTGTTCAGGAGGA 420
QY 442 AATCCCGCTGTTAATACCCCGGGGATGACAGTACCBGAAGAATAAGCACCGGCTAAC 501
DB 421 AATCATTCTGGCTAATACCCCGGAGTGGATACCGTACCGGAAGAATAAGCACCGGCTAAC 480
QY 502 TAGTGCAGCAGCCGCGGTAAATACGTAGGTGCAAGCGTTAATCGGAATTTACTGGGCGT 561
DB 481 TACGTGCAGCAGCCGCGGTAAATACGTAGGTGCGAGCGTTAATTTGGAAATTTACTGGGCGT 540
QY 562 AAAGCTGCGCAGCGGTTTTTCAAGTCTGATGTGAAAGCCCGGGCTCAACCTGGGAAAC 621
DB 541 AAAGCTGCGCAGCGGTTTTCTAAGACCGATGTGAATCCCGGGCTCAACCTGGGAAAC 600
QY 622 GGCATTGGAGACTGCAAGACTAGAGTGGTTCAGAGGGGGGTAGAAATTCGCGGTGTAGCAG 681
DB 601 TGCAATTGGTACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAAATTCACGTTAGCAG 660
QY 682 TGAATGCTGATGATGCGGAGGAATACCGATGGGGAAGGCGCCCTCGGGATGACACT 741
DB 661 TGAATGCTGATGATGCGGAGGAATACCGATGGGGAAGGCGCCCTCGGGCAATACT 720
QY 742 GACGCTCATGCAGAAACGCTGGGAGCAACACAGGATTAGATACCTCGTGTAGTCCACGCC 801
DB 721 GACGCTCATGCAGAAACGCTGGGAGCAACACAGGATTAGATACCTCGTGTAGTCCACGCC 780
QY 802 CTAAACGATGTAATAGTCTGTGGGGGTTTGAATCTCTTGGTGTAGGTAGCTTAACCGCTGA 861
DB 781 CTAAACGATGTAATAGTCTGTGGGGGTTTGAATCTCTTGGTGTAGGTAGCTTAACCGCTGA 840
QY 862 AATTGACCGCTGGGAGTACGGCGCAAGGTTAAACCTCAAGGAATTTGACGGGACCC 921
DB 841 AGTTGACCGCTGGGAGTACGGTTCGAAGATTAAACCTCAAGGAATTTGACGGGACCC 900

RESULT 10

WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490

WP	Fragment Name	Begin	End
WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000
WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668
ID	AAA81490 standard; DNA; 1437668 BP.		
XX	AAA81490;		
AC	AAA81490;		
XX	04-DEC-2000 (first entry)		
DT			
XX			
DE	N. meningitidis B full length genome DNA sequence SEQ ID NO:1068.		
XX			
KW	Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;		
KW	antigen; vaccine; diagnosis; infection; antibacterial; identification;		
KW	Meningococcus B; MenB; ds.		
XX			
OS	Neisseria meningitidis.		
XX			
PN	WO2000022430-A2.		
XX			
PD	20-APR-2000.		
XX			
PF	08-OCT-1999; 99WO-US023573.		
XX			
PR	09-OCT-1998; 98US-0103794P.		
PR	30-APR-1999; 99US-0132068P.		
XX			
PA	(CHIR) CHIRON CORP.		
XX			
FI	Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;		
PI	Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;		
PI	Rappuoli R, Pizza M;		
XX			
DR	WPI; 2000-318079/27.		
XX			
PT	Isolated nucleotide sequences of Neisseria meningitidis which can be used		
PT	in the diagnosis and treatment of N. meningitidis infection and other		
PT	Neisserial infections, for example, N.gonorrhoea.		
XX			
PS	Claim 7; Page 866-1272; 1760pp; English.		
XX			
CC	The present invention describes methods of obtaining immunogenic proteins		
CC	from Neisseria genomic sequences. AAA81453 to AAA82414 represent		
CC	specifically claimed Neisseria meningitidis genomic DNA sequences:		
CC	AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA		
CC	sequences and their corresponding proteins; AAA81254 to AAA81259 and		
CC	AAA81304 to AAA81321 represent PCR primers used in the isolation of		
CC	Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent		
CC	Neisseria meningitidis MenB polynucleotide ORF sequences, which are all		
CC	used in the exemplification of the present invention. The nucleic acid		
CC	sequences, protein sequences, and antibodies against them, can be used in		
CC	the manufacture of a composition. The composition can be used as a		
CC	medicament (or in the manufacture of a medicament) for treating,		
CC	preventing or diagnosing infection due to Neisserial bacteria. For		
CC	example, some of the identified proteins could be components of vaccines		
CC	against Meningococcus B; against all serotypes; and/or against all		
CC	pathogenic Neissariae. Identification of sequences from the bacterium		
CC	will also facilitate production of biological probes, particularly		
CC	organism-specific probes. Attempts to make efficacious Meningococcus B		
CC	vaccines have failed mainly due to antigen tolerance. Multivalent		
CC	vaccines have also been tried but none have successfully overcome		

Qy	118	GAATGTTACCGTCTTAATGGGGGATAGCTCGGCGAAAGCCGGATTAAATACCCATACGCCCT	177
Db	107842	GAACCTACCGAGTAGTGGGGGATACTGATCGAAAGATACGCTAAATACCGCATACGCTTT	107901
Qy	178	GAGGGGAAGCCGGGAGTCCAAAGACCTCGCGTTATACGAGCAGCCGAGCTCTGATTAG	237
Db	107902	GAGAGAAAGCAGGGGACCTTCGGGCTTCGCGTATTCGAGCGCGGATATCTGATTAG	107961
Qy	238	CTAGTTGGTGAAGTAAGAGCTCACAAAGGGGACCATCAGTAGCGGGTCTCAGAGGATGAT	297
Db	107962	CTAGTTGGTGGGTAAAGGCTTACCAAGGGGACCATCAGTAGCGGGTCTCAGAGGATGAT	108021
Qy	298	CCGCGACACTCTGGGACTGAGACACGGCCACAGTCTCTACGGAGGACAGCTGGGGAAATTT	357
Db	108022	CCGCGACACTGGGACTGAGACACGGCCACAGTCTCTACGGAGGACAGCTGGGGAAATTT	108081
Qy	358	TGGACATGGGGCAACCTGATCCAGCGATGCCGCTGTCTGAAGAGGCCCTTCGGGTT	417
Db	108082	TGGACATGGGGCAAGCCTGATCCAGCGATGCCGCTGTCTGAAGAGGCCCTTCGGGTT	108141
Qy	418	GTAAGGACTTTTGTCAAGGAGGAAATCCCGCTGTTTAATACCCGGCGGGGATCACAGTA	477
Db	108142	GTAAGGACTTTTGTCAAGGAGGAAAGGCTGTGTCTTAATATCAGCGCTGATGACGGTA	108201
Qy	478	CCBGAAGAAATAGCACCGGCTAACTACGTGCCAGCAGCCGGGTAAATACGTAGGGTGCAA	537
Db	108202	CCTGAAGAAATAGCACCGGCTAACTACGTGCCAGCAGCCGGGTAAATACGTAGGGTGCGA	108261
Qy	538	GCGTTAATCCGAATTAAGTGGCGTAAAGCGTGGCAGCGGCTTTGCAAGTCTGATGTA	597
Db	108262	GCGTTAATCCGAATTAAGTGGCGTAAAGCGGCGCAGCGGTTACTTTAAGCAGGATGTA	108321
Qy	598	AAGCCCGGGCTCAACCTGGGAAACGGCATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGG	657
Db	108322	AATCCCGGGCTCAACCCGGGACTGCTTCTGNACTGGGTGACTCAGTGTGTGAGAGG	108381
Qy	658	GGGTAGAAATCCCGTGTAGCAGTGAATTCGCTAGAGATGCGGAGGAATACCGATGGCG	717
Db	108382	GAGGTAGAAATCCACGTGTAGCAGTGAATTCGCTAGAGATGTCGAGGAATACCGATGGCG	108441
Qy	718	AAGCGACCCCTGGGATGACACTGACCTCATGTCACGAAGCGTGGGGAGCAACAGGA	777
Db	108442	AAGCGACCCCTGGGAGCAACACTGACCTCATGTCGCGAAGCGTGGGTAGCAACAGGA	108501
Qy	778	TTAGATACCTCTGTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTGGG-GGTTTGAAT	836
Db	108502	TTAGATACCTCTGTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTGGGCAACCTGAT	108561
Qy	837	CCTTGTAGCGTACGTTAACCGGTGAATTCACCGCTTGGGGAGTACGGCCGCAAGGTAA	896
Db	108562	GCTTGTAGCGTACGTTAACCGGTGAATTCACCGCTTGGGGAGTACGGTCGCAAGATTAA	108621
Qy	897	AACCTCAAGGAATGACGGGACCCGACAAAGCGGTGGATGATGTGGATTAATTCGATGC	956
Db	108622	AACCTCAAGGAATGACGGGACCCGACAAAGCGGTGGATGATGTGGATTAATTCGATGC	108681
Qy	957	AACGCGAAAACTTACTCTCTTGAATGATGCGGAACTTGTGTAGAGATATCTTGTGTC	1016
Db	108682	AACGCGAAGAACTTACTCTCTTGAATGATGCGGAACTTGTGTAGAGATATCTTGTGTC	108739
Qy	1017	CCGAAAGGGAGCCGTAAACAGGTGTGCAATGCTGTCGTCAGCTCGTGTGTCGATGATGT	1076
Db	108740	GCCTTCGGGAGCCGTAAACAGGTGTGCAATGCTGTCGTCAGCTCGTGTGTCGATGATGT	108799
Qy	1077	TGGGTTAAGTCCCGCAACGAGCCGACCCCTTGTCAATTAGTTGCCATCATTTAGTTGGCA	1136
Db	108800	TGGGTTAAGTCCCGCAACGAGCCGACCCCTTGTCAATTAGTTGCCATCATTTAGTTGGCA	108859
Qy	1137	CTCTAATGAGACTGCGGTCACAAAACGGAGGAGGTGGGGATGACGCTCAAGTCCCTCATG	1196
Db	108860	CTCTAATGAGACTGCGGTCACAAAACGGAGGAGGTGGGGATGACGCTCAAGTCCCTCATG	108919
Qy	1197	GCCTTTATGAGCAGGGGCTTCCACAGTCATCAATATGCTCGGTACAGAGGGTTCGTAAGCCG	1256

Db	108920	GCCTTTATGACCAAGGGCTTCACACGTCATCAATATGCTCGGTACAGAGGGTAGCAAGCCG	108979
Qy	1257	CGAGGTGGTGCCTAATCTCATAAACCGATCGTAGTCCGGATCCGACTCTCCTCACTCGAGT	1316
Db	108980	CGAGGCGGAGCCAAATCTCAAAACCGATCGTAGTCCGGATTCGACTCTCCTCACTCGAGT	109039
Qy	1317	GCCTGAAGTCGGAATCGCTAGTAAATCGCAGATCAGCATGCTGGGTGAATACGTTCCCGG	1376
Db	109040	GCATGAAGTCGGAATCGCTAGTAAATCGCAGGTGAGCATCTCGGTGAATACGTTCCCGG	109099
Qy	1377	GTCTTGTACACACCGCCGCTCACCATGGAATGAGTTTCCACAGAGTGGGTAGGCTA	1436
Db	109100	GTCTTGTACACACCGCCGCTCACCATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT	109159
Qy	1437	ACC 1439	
Db	109160	ACC 109162	

RESULT 12

AAA81490_03

Continuation (4 of 15) of AAA81490 from base 300001 (N. meningitidis B full length genome)

WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490

WP	Fragment Name	begin	end
WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000
WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668

Query Match 80.5%; Score 1159; DB 3; Length 110000;

Best Local Similarity 89.1%; Pred. No. 0;

Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;

Qy	4	AGAGTTTGTATCCTGGCTCAGATTGAACGCTGGCGGATGCTTTACACATCGAAGTCGAC	63
Db	7722	AGAGTTTGTATCCTGGCTCAGATTGAACGCTGGCGGATGCTTTACACATCGAAGTCGAC	7781
Qy	64	GGTA-----ACAGGTTGCTTGCCACCGCTGACGAGTGGCGAAACGGGTGAGTAATTCGCTCG	117
Db	7782	GGCAGCACAGAGAGCTTCTCTCGGTGGCGAGTGGCGAACGGGTGAGTAATTCG	7841
Qy	118	GAATGTACCGTGTAAATGGGGATGAGTCCGCGAAACCGGATTAATACCGCATACGCCCT	177
Db	7842	GAACGTACCGGATGAGTGGGGATTAATCTGATCGAAGATCAGCTAATACCGCATACGCCCT	7901
Qy	178	GAGGGGAAGCGGGGATCGAAGACCTCGCGTTATACGACGACCGGCTCTGATTAG	237
Db	7902	GAGAGAGAAGCAGGGGATCTTCGGGCTTTCGCTAATTCGAGCGCGGATATCTGATTAG	7961
Qy	238	CTAGTTTGTGAGTGAAGCTCACCAAGGCGACGATCAGTAGCGGCTCTGAGAGGATGAT	297
Db	7962	CTAGTTTGTGGGTAAAGGCTTACCAGGCGACGATCAGTAGCGGCTCTGAGAGGATGAT	8021
Qy	298	CGGCCACACTGGGACTGAGACACGGCCAGACTCTTACGGGAGGACGAGTGGGGAAATTT	357
Db	8022	CGGCCACACTGGGACTGAGACACGGCCAGACTCTTACGGGAGGACGAGTGGGGAAATTT	8081
Qy	358	TGGACAAATGGGGCAACCTGATCCAGCCATGCCGCTGTCTGAAAGAGCCCTTCGGGTT	417
Db	8082	TGGACAAATGGGGCAACGCTGATCCAGCCATGCCGCTGTCTGAAAGAGCCCTTCGGGTT	8141

Qy 418 GTAAGGACTTTTCTCAGGGAGGAATCCCGCTGGTTAATACCCGCGGGGATGACAGTA 477
Db 8142 GTAAAGGACTTTTGTGAGGGAAGAAAAGGCTGTGCTAAATATCAGCGGCTGATACCGGTA 8201
Qy 478 CCBGAAGAATAAGCAACCGGCTAACTAGTGTCCAGCAGCCGCGGTAAATACGTAGGGTGCAA 537
Db 8202 CCTGAGNATTAAGCAACCGGCTAACTAGTGTCCAGCAGCCGCGGTAAATACGTAGGGTGCGA 8261
Qy 538 GCGTTAATCGGAATTACTTGGGCGTAAAGCGGTGCGAGCGCGGTTTTGCAAGTCTCATGTGA 597
Db 8262 GCGTTAATCGGAATTACTTGGGCGTAAAGCGGCGCAGACGGTTACTTTAAGCAGCATGTGA 8321
Qy 598 AAGCCCCGGGCTCAACTGGGAACGGCATTTGGAGACTTCAAGACTAGAGTCCGTCAGAGG 657
Db 8322 AATCCCCGGGCTCAACCGGGAATGCGGTTCTGAACCTGGGTGACTCGAGTGTGCAGAGG 8381
Qy 658 GGGGTAGAAATCCCGGTGTAGCAGTGAATACGCTAGAGATCCGAGGAATAACCGATGGCG 717
Db 8382 GAGGTAGAAATCCAGGTGTAGCAGTGAATACGCTAGAGATGTGGAGNATACCGATGGCG 8441
Qy 718 AAGCAGCCCCCTGGGATGACACTGACGCTCATGCAAGAAAGCGTGGGGAGCAAAACAGGA 777
Db 8442 AAGCAGGCTCTCTGGGACAACTGACGTTTATGCCCCGAAGCGTGGGTAGCAAAACAGGA 8501
Qy 778 TTAGATACCCCTGGTAGTCAAGCTTAACCGATGTCAATTAGCTGTTGGG-GGTTTGAAT 836
Db 8502 TTAGATACCCCTGGTAGTCAAGCTTAACCGATGTCAATTAGCTGTTGGGCAAACCTGATT 8561
Qy 837 CTTTGGTAGCGTAGCTAACCGGTGAAATTTGACCGCTGGGGAGTACGGCCCAAGGTTAA 896
Db 8562 CTTTGGTAGCGTAGCTAACCGGTGAAATTTGACCGCTGGGGAGTACGGTCCGAGATTAA 8621
Qy 897 AACTCAAGGAATTAAGCGGGACCGCAACAGCGGTGGATGATGTGGAAATTAATTCGATGC 956
Db 8622 AACTCAAGGAATTAAGCGGGACCGCAACAGCGGTGGATGATGTGGAAATTAATTCGATGC 8681
Qy 957 AACGGGAAAACCTTACCTGCTCTTGACATGTCAGAACTTGGTAGAGATATCTTGTGTC 1016
Db 8682 AACCGGAAGAACCCTTACCTGCTCTTGACATGTCAGAA--TCCTCCGGAGACGGAGGAGT 8739
Qy 1017 CCGAAAGGAGCGGTAAACAGAGGTGCTGATGGCTGTGCTCAGCTCGTGTGCTGAGATGT 1076
Db 8740 GCCTTCGGGAGCGGTAAACAGAGGTGCTGATGGCTGTGCTCAGCTCGTGTGAGATGT 8799
Qy 1077 TGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCCATCAATTTAGTTGGGCA 1136
Db 8800 TGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCCATCAATTCAGTTGGGCA 8859
Qy 1137 CTCTAATGAGACTGCGGTGACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCATG 1196
Db 8860 CTCTAATGAGACTGCGGTGACAAACCGGAGGAGGAGGTGGGATGACGTCAAGTCTCATG 8919
Qy 1197 GCGCTTATGAGCAGGCGTTCACAGCTCATACAATGGTCCGTACAGAGGCTCGCTAAGCCG 1256
Db 8920 GCGCTTATGACAGGCGTTCACAGCTCATACAATGGTCCGTACAGAGGAGGTAGCAAGCCG 8979
Qy 1257 CGAGTGTGTGCAATCTCATAAAACCGATCGTGTGTCGGATGCGACTCTGCAACCTCGAGT 1316
Db 8980 CGAGGCGGACCAATCTCAAAAACCGATCGTGTGTCGGATGCGACTCTGCAACCTCGAGT 9039
Qy 1317 GCGTGAAGTCCGAATCCGTAGTAAATCCGAGATCAGCATGCTGCGGTGAATAGTTCCCGG 1376
Db 9040 GCATGAAGTCCGAATCCGTAGTAAATCCGAGATCAGCATGCTGCGGTGAATAGTTCCCGG 9099
Qy 1377 GTCTTTGTACACACCGCCGTCACACCATGGGAGTCAAGTTTCAACGAAAGTGGGTAGGCTA 1436
Db 9100 GTCTTTGTACACACCGCCGTCACACCATGGGAGTGGGAGTACGAGAGTAGTAGGATA 9159
Qy 1437 ACC 1439
Db 9160 ACC 9162

RESULT 13
AAA81489_2/c
Continuation (3 of 9) of AAA81489 from base 200001 (N. meningitidis partial DNA sequence
WP Sequence split into 9 fragments LOCUS AAA81489 Accession AAA81489
Fragment Name Begin End
WP AAA81489_0 1 110000
WP AAA81489_1 100001 210000
WP AAA81489_2 200001 310000
WP AAA81489_3 300001 410000
WP AAA81489_4 400001 510000
WP AAA81489_5 500001 610000
WP AAA81489_6 600001 710000
WP AAA81489_7 700001 810000
WP AAA81489_8 800001 837096
Query Match 80.5%; Score 1159; DB 3; Length 110000;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;
Qy 4 AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAAC 63
Db 95302 AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACATGCAAGTCGAC 95243
Qy 64 GGTA-----ACAGGGTGTCTTGACCCGCTGACAGTGGCGAAACGGGTGAGTAAATGCGTCG 117
Db 95242 GGCAGCACAGAGAAGCTTGCTTCTCGGTGCGAGTGGCGAACGGGTGAGTAAACATATCG 95183
Qy 118 GAATGTACCGTGTAAATGGGGATAGCTCGCGGAAAGCCGGAATTAATACCGATACGCGCT 177
Db 95182 GAACGTACCGAGTAGTGGGGATAACTGATCGAAAGATCAGCTAAATCCGATACGCTT 95123
Qy 178 GAGGGGAAAGCGGGGATCGAAAGACCTCGCTTATACAGAGCAGCGAGCTCTGATTAG 237
Db 95122 GAGAGAAAGCAGGGGACCTTCGGGCTTTCGGCTATTCAGCGCCGATATCTGATTAG 95063
Qy 238 CTAGTTGCTGAGGTAAAGAGTCTACCAAGGGCAGCATCAGTAGCGGGTCTGAGAGGATGAT 297
Db 95062 CTAGTTGCTGAGGTAAAGAGTCTACCAAGGGCAGCATCAGTAGCGGGTCTGAGAGGATGAT 95003
Qy 298 CCGCCACACTGGGACTGAGACACGCGCCAGACTCTTACGGGAGCAGCAGTGGGGAATTT 357
Db 95002 CCGCCACACTGGGACTGAGACACGCGCCAGACTCTTACGGGAGCAGCAGTGGGGAATTT 94943
Qy 358 TGGCAATGGGGCAACCCGTATCCAGCATGCCGCTGTCTGAAGAGGCTTTCGGGTT 417
Db 94942 TGGCAATGGGGCGCAAGCCTGATCCAGCATGCCGCTGTCTGAAGAGGCTTTCGGGTT 94883
Qy 418 GTAAAGGACTTTTCTCAGGGAGGAATAATCCCGCTGGTTAATAACCGCGGGGATGACAGTA 477
Db 94882 GTAAAGGACTTTTCTCAGGGAGGAATAATCCCGCTGGTTAATAATCAGCGGCTGATGACGTA 94823
Qy 478 CCBGAAGAATAAGCAACCGGCTAACTAGTGTCCAGCAGCCGCGGTAAATACGTAGGGTGCAA 537
Db 94822 CCTGAAGAATAAGCAACCGGCTAACTAGTGTCCAGCAGCCGCGGTAAATACGTAGGGTGCGA 94763
Qy 538 GCGTTAATCGGAATTACTTGGGCGTAAAGCGTCCAGCGGCTTTTGGCAAGTCTGATGTA 597
Db 94762 GCGTTAATCGGAATTACTTGGGCGTAAAGCGGCGCAGACGGTTACTTAAAGCAGGATGTA 94703
Qy 598 AAGCCCCGGGCTCAACCTTGGGAACGGCATTTGGAGACTGCAAGACTTAGAGTCCGTCAGAGG 657
Db 94702 AATCCCCGGGCTCAACCCGGGAACCTGCGTTCTGAACTGGGTGACTCGAGTGTGTCAGAGG 94643
Qy 658 GGGGTAGAAATCCCGGTGTAGCAGTGAATCCGTAGAGATCGGAGGAAATACCGATGGCG 717
Db 94642 GAGGTAGAAATCCACGTGTAGCAGTGAATCCGTAGAGATCGGAGGAAATACCGATGGCG 94583
Qy 718 AAGCAGCCCCCTGGGATGACACTGACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGA 777
Db 94582 AAGCAGGCTCTCTGGGACAACTGACGTTTATGCCCCGAAGCGTGGGTAGGAGTACGAAACAGGA 94523
Qy 778 TTAGATACCCCTGGTAGTCCAGCCCTAAACGATGTCAATTAGCTGTTCGGG-GGTTTGAAT 836
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Db 94522 TTAGATACCCCTGGTAGTCCAGCCCTAAACGATGTCAATTAGCTGTTGGGCAACCTGATT 94463
Qy 837 CCTTGGTAGCTAGCTAAACGGTGAATTTGACCGCTCGGGAGTAGCGCCCAAGGTTAA 896
Db 94462 CCTTGGTAGCTAGCTAAACGGTGAATTTGACCGCTCGGGAGTAGCGTCCCAAGATTAA 94403
Qy 897 AACTCAAAGGAATTGAACGGGACCGCAACAGCGGTGGATGATGGATTAAATTCGATGC 956
Db 94402 AACTCAAAGGAATTGAACGGGACCGCAACAGCGGTGGATGATGGATTAAATTCGATGC 94343
Qy 957 AACGGAAAAACCTTACTGCTCTTTGACATGTACGGAACTTGGTAGAGATATCTTGGTGC 1016
Db 94342 AACCGAAGAACCTTACTGCTCTTTGACATGTACGGAA--TCCTCCGAGCGGAGGT 94285
Qy 1017 CCGAAAGGAGCGGTAAACACAGGTGCTGCATGGCTGTCTGCTCAGCTCGTGTGCTGAGATGT 1076
Db 94284 GCCTTCGGGAGCGGTAAACACAGGTGCTGCATGGCTGTCTGCTCAGCTCGTGTGCTGAGATGT 94225
Qy 1077 TGGGTTAAGTCCCGCAACGAGCGCAACCTTTGTCAATTAGTTGCCATCATTTAGTTGGGCA 1136
Db 94224 TGGGTTAAGTCCCGCAACGAGCGCAACCTTTGTCAATTAGTTGCCATCATTCAGTTGGGCA 94165
Qy 1137 CTCTAATGAGACTGCGCGTGAACAGCGGAGGAGTGGGATGACGTCGATCAAGTCTCTCATG 1196
Db 94164 CTCTAATGAGACTGCGCGTGAACAGCGGAGGAGTGGGATGACGTCGATCAAGTCTCTCATG 94105
Qy 1197 GCCCTTATGACAGCGGCTTACACGTTCATCAATGCTGCGGTACAGAGGTCGCTAAGCCG 1256
Db 94104 GCCCTTATGACAGCGGCTTACACGTTCATCAATGCTGCGGTACAGAGGTCGCTAAGCCG 94045
Qy 1257 CGAGGTGGTCCCAATCTCATAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGT 1316
Db 94044 CGAGGCGAGGCCAATCTCAAAAACCGATCGTAGTCCGGATTCGCACTCTGCAACTCGAGT 93985
Qy 1317 GCGTGAAGTCGGAATCGCTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGG 1376
Db 93984 GCATGAAGTCGGAATCGCTAGTAATCGCAGTCAAGCATCTGCGGTGAATACGTTCCCGG 93925
Qy 1377 GTCTTTGACACACCGCGCTCACACCATGGAGTGAGTTTCACACAGAGTGGGTAGGCTA 1436
Db 93924 GTCTTTGACACACCGCGCTCACACCATGGAGTGGGGATACCAGAAGTAGGTAGGATA 93865
Qy 1437 ACC 1439
Db 93864 ACC 93862
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RESULT 14

AAA81489_6/c

Continuation (7 of 9) of AAA81489 from base 600001 (N. meningitidis partial DNA sequence
WP Sequence split into 9 fragments LOCUS AAA81489 Accession AAA81489

WP	Fragment Name	Begin	End
WP	AAA81489_0	1	110000
WP	AAA81489_1	100001	210000
WP	AAA81489_2	200001	310000
WP	AAA81489_3	300001	410000
WP	AAA81489_4	400001	510000
WP	AAA81489_5	500001	610000
WP	AAA81489_6	600001	710000
WP	AAA81489_7	700001	810000
WP	AAA81489_8	800001	837096

Query Match 80.5%; Score 1159; DB 3; Length 110000;

Best Local Similarity 89.1%; Pred. No. 0; Mismatches 147; Indels 9; Gaps 3;
Matches 1286; Conservative 1;

Qy	4	AGAGTTTGATCCTGGCTCAGATTGAACGCTCGGGCATGCTTTACACATGCAAGTCCGAAC	63
Db	102173	AGAGTTTGATCCTGGCTCAGATTGAACGCTCGGGCATGCTTTACACATGCAAGTCCGAC	102114
Qy	64	GGTA-----ACAGGTGCTTGCACCGCTACGAGTGGCGAACCGGTGAGTAATGCGTCG	117
Db	102113	GGCAGCACAGAGAAGCTTGCTTCTCGGTGCGGAGTGGCGAACCGGTGAGTAATGCTCATATCG	102054

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QY	1257	CGAGTGTGTGCAATCTCATAAACCCGATCCGTAGTCCGGATCGCACTCTGCAACTCGAGT	1316
Db	100915	CGAGGCGAGCCATCTCACAACCCGATCCGTAGTCCGGATCGCACTCTGCAACTCGAGT	100856
QY	1317	CGGTGAAGTCGGAATCGTCTAGTAATCGCAGATACGATCTGCGGTGAATACGTTCCGG	1376
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Db	100735	ACC 100733	
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WP Sequence split into 9 fragments LOCUS AAA81489 Accession Aaa81489			
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WP	AAA81489_2	200001	310000
WP	AAA81489_3	300001	410000
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WP	AAA81489_5	500001	610000
WP	AAA81489_6	600001	710000
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Best Local Similarity 80.5%; Score 1159; DB 3; Length 110000;			
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;			
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QY	178	GAGGGGAAAGCGGGGATCGAAAGACCTTCGGCTTATACGAGCAGCCGACGTCGATTAG	237
Db	1993	GAGAGAAAGCAGGGACCTTCGGCCCTTGCGCTATTCGAGCGCCGATATCTGATTAG	1934
QY	238	CTAGTTGTGAGGTAAAGACTCACCAAGCGACGATCAGTACGGGGTCTGAGAGATGAT	297
Db	1933	CTAGTTGTGGGTAAAGCCCTACCAAGCGCAGATCAGTACGGGGTCTGAGAGGATGAT	1874
QY	298	CCGCCACTGGGACTGAGACACGGCCAGACTCTCTACGGGAGGACGAGTGGGGAATT	357
Db	1873	CCGCCACTCTGGGACTGAGACACGGCCAGACTCTCTACGGGAGGACGAGTGGGGAATT	1814
QY	358	TGGACAATGGGGCAACCCCTGATCCAGCCATCCCGCTGTCTGAAGAAGGCCCTTCGGGTT	417
Db	1813	TGGACATGGGCGAAGCCTGATCCAGCCATCCCGCTGTCTGAAGAAGGCCCTTCGGGTT	1754
QY	418	GTAAGGACTTTTGTGACGGAGGAATCCCGTGTGTTAATACCCGGCGGGGATGACAGTA	477
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QY	478	CCBGAAGATAAGCACCGCGCTTAACGTACGTGCCAGCAGCCGCGTAAATACGTAGGTTGCAA	537

Search completed: May 23, 2006, 23:28:15
Job time : 985 secs

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QY	778	TTAGATACCCCTGGTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTTGGG-GGTTTGAAT	836
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QY	957	AACCGGAARACCTTACTGCTCTTTCATGTCATGTCGGAACCTTGGTAGAGATATCTTGGTGC	1016
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QY	1437	ACC 1439	
Db	735	ACC 733	

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 00:50:35 ; Search time 1994 Seconds
(without alignments)
8873.719 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1439.2	100.0	1440	10	US-10-678-023-1
2	1180	82.0	1522	16	US-11-198-242-2
3	1169.6	81.3	1610	7	US-10-029-397A-43
4	1165.8	81.0	1460	7	US-10-168-337A-6
5	1161.6	80.7	1532	7	US-10-029-397A-38
6	1160.6	80.6	1460	7	US-10-168-337A-4
7	1159.8	80.6	1488	7	US-10-029-397A-42
8	1159	80.5	1460	7	US-10-168-337A-2
9	1159	80.5	1544	7	US-10-029-397A-45
10	1159	80.5	2242716	10	US-10-915-740A-1068
11	1159	80.5	2242716	10	US-10-915-740A-1068
12	1157.6	80.4	1460	7	US-10-168-337A-1
13	1152	80.0	1544	3	US-09-726-774-5
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16	1150	79.9	1459	7	US-10-168-337A-8
17	1149.8	79.9	1478	7	US-10-168-337A-3

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19	1149	79.8	1458	8	US-10-659-980A-3	Sequence 3, Appli
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21	1148.4	79.8	1426	7	US-10-168-337A-9	Sequence 9, Appli
22	1147.6	79.7	1464	7	US-10-029-397A-40	Sequence 40, Appli
23	1147.6	79.7	1485	7	US-10-168-337A-10	Sequence 10, Appli
24	1146.8	79.7	1535	7	US-10-029-397A-41	Sequence 41, Appli
25	1137	79.0	1485	7	US-10-029-397A-39	Sequence 39, Appli
26	1135	78.9	20844	10	US-10-915-740A-8	Sequence 8, Appli
27	1126.8	78.3	1496	10	US-10-723-365B-32	Sequence 32, Appli
28	1126	78.2	1530	9	US-10-875-161-1	Sequence 1, Appli
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30	1119.4	77.8	1508	16	US-11-248-383-1	Sequence 1, Appli
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33	1115.6	77.5	1491	8	US-10-659-980A-20	Sequence 20, Appli
34	1115.6	77.5	1491	8	US-10-659-983A-20	Sequence 20, Appli
35	1104.4	76.7	1494	8	US-10-659-948A-19	Sequence 19, Appli
36	1104.4	76.7	1494	8	US-10-659-980A-19	Sequence 19, Appli
37	1104.4	76.7	1494	8	US-10-659-983A-19	Sequence 19, Appli
38	1103	76.6	1457	8	US-10-659-948A-1	Sequence 1, Appli
39	1103	76.6	1457	8	US-10-659-980A-1	Sequence 1, Appli
40	1103	76.6	1457	8	US-10-659-983A-1	Sequence 1, Appli
41	1099.8	76.4	1457	8	US-10-659-948A-2	Sequence 2, Appli
42	1099.8	76.4	1457	8	US-10-659-980A-2	Sequence 2, Appli
43	1099.8	76.4	1457	8	US-10-659-983A-2	Sequence 2, Appli
44	1098.4	76.3	1467	8	US-10-659-948A-18	Sequence 18, Appli
45	1098.4	76.3	1467	8	US-10-659-980A-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1

US-10-678-023-1
; Sequence 1, Application US/10678023
; Publication No. US20050074431A1
; GENERAL INFORMATION:
; APPLICANT: Martin et al., Phyllis A. W.
; TITLE OF INVENTION: CHROMOBACTERIUM SUTTSUGA SP. NOV. AND USE FOR CONTROL OF INSECT
; FILE REFERENCE: 0136.02
; CURRENT APPLICATION NUMBER: US/10/678,023
; CURRENT FILING DATE: 2003-10-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Chromobacterium suttsuga NRRL B-30655
US-10-678-023-1

Query Match 100.0%; Score 1439.2; DB 10; Length 1440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-11-198-242-2
; Sequence 2, Application US/11198242
; Publication No. US20060035345A1
; GENERAL INFORMATION:
; APPLICANT: AJINOMOTO CO., INC.
; TITLE OF INVENTION: Process for the production of beta-amino acids by using acylase
; FILE REFERENCE: AB04037
; CURRENT APPLICATION NUMBER: US/11/198,242
; CURRENT FILING DATE: 2005-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Burkholderia sp.
; FEATURE:
; NAME/KEY: 16S rDNA
; LOCATION: (1)..(1522)
; OTHER INFORMATION:
; US-11-198-242-2

Query Match 82.0%; Score 1180; DB 16; Length 1522;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 1283; Conservative 1; Mismatches 147; Indels 5; Gaps 1;
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Qy 1201 TTATGACGAGGGCTTCACAGTCAATACAAATGGTCCGTACAGAGGTGCTTAAGCCGCGAG 1260
Db 1254 TTATGGGTAGGGCTTCACAGTCAATGGTCCGAAACAGAGGTGCGCAACCCGCGAG 1313
Qy 1261 GTGTGCCAATCTCATAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGT 1320
Db 1314 GGGGAGCCAAATCCAGAAAACCGATCGTAGTCCGGATTCGCAACTCGAGTGGAT 1373
Qy 1321 GAAGTCCGAAATCGCTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGGTCT 1380
Db 1374 GAAGCTGGATCGCTAGTAATCGCGGATCAGCATGCGCGGTGAATACGTTCCCGGGTCT 1433
Qy 1381 TGTACACACCCCGCTCACACATCGGAGTGGAGTTCACACAGAGTGGTAGGCTAACCG 1440
Db 1434 TGTACACACCCCGCTCACACATCGGAGTGGGTTTACACAGAGTGGCTAGTCTAACCG 1493

RESULT 4
US-10-168-337A-6
; Sequence 6, Application US/10168337A
; Publication No. US20030170654A1
; GENERAL INFORMATION:
; APPLICANT: Crocetti, Gregory R.; Tyson, Gene W.; Hugenholz, Philip; and Blackall,
; APPLICANT: Linda L.
; TITLE OF INVENTION: Probes and Primers for the Detection of Polyphosphate
; TITLE OF INVENTION: Accumulating Organisms in Wastewater
; FILE REFERENCE: 002367PC/KF
; CURRENT APPLICATION NUMBER: US/10/168.337A
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:
; OTHER INFORMATION: Polyphosphate-accumulating organism
US-10-168-337A-6

Query Match 81.0%; Score 1165.8; DB 7; Length 1460;
Best Local Similarity 89.3%; Pred. NO. 0;
Matches 1267; Conservative 1; Mismatches 149; Indels 2; Gaps 1;

Qy 24 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAAACGGTAACAGGGTGTTCGACCC 83
Db 1 ATTTAAACGCTGGCGCATGCTTTACACATGCAAGTCGAAACGGTAACAGGGTGTTCGACCC 60
Qy 84 GCTGACGAGTGGCGAACCGGTGAGTAAATGCTCGGAATGTACCGTGTAAATCGGGGATAGC 143
Db 61 GGTGCGGAGTGGCGAACCGGTGAGTAAATGCTCGGAACGCTCGAAGTGGGGGATAAC 120
Qy 144 TCGGGAAGCCGGATTAATACCGATACGCCCTGAGGGGGAAGACCGGGGATCGAAGA 203
Db 121 CGACGGAAGCTTACGCTTAATACCGCATATTCTGTGAGCAGGAAAGCAGGGGATCGCAAGA 180
Qy 204 CCTCGGTTATACGAGACCGACGCTCTGATTAGTCTGAGTGGTGAAGAGTCTCACCA 263
Db 181 CTTTGGCTTTGGGAGCGCCGATGTCGGAATTAGTCTGTTGGTGGGTAAATGGCTTACCA 240
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Qy 264 AGCGGCGATCAGTACGGGTCTGAGAGGATGATCCGCCACACTTGGGACTGAGACACGGC 323
Db 241 AGCGGCGATCCGCTAGCGGTCTGAGAGGATGATCCGCCACACTTGGGACTGAGACACGGC 300
Qy 324 CCAGACTCCTTACCGGAGGACGAGTGGGAAATTTTGGCAATGGGGCAACCCCTGATCCA 383
Db 301 CCAGACTCCTTACCGGAGGACGAGTGGGAAATTTTGGCAATGGGGCAACCCCTGATCCA 360
Qy 384 GCATGCGCGTGTCTGAAAGAGCCCTTGGGTTGTAAGGACTTTTGTTCAGGAGGAAA 443
Db 361 GCCATGCGCGGTGAGTGAAAGAGCCCTTGGGTTGTAAGGACTTTTGGGCGGGAAGAAA 420
Qy 444 TCCGCTGGTTAATACCCGCGGGGATGACAGTACCBGAAGAATAGCACCGGCTACTA 503
Db 421 TTGCTTTGGGTTAATACCCCTGAGTAGATGACGTTACCGAATAAGAACACCGGCTAACTA 480
Qy 504 CGTCCAGACAGCCCGGTAAATAGTAGGGTCAAGCGTTAATCGGAATTAATCGGGCGTAA 563
Db 481 CGTCCAGACAGCCCGGTAAATAGTAGGGTCAAGCGTTAATCGGAATTAATCGGGCGTAA 540
Qy 564 AGCTGGCAGGCGGTTTTCGAAAGTCTGATGTGAAAGCCCGGGCTCAACCTGGGAACGG 623
Db 541 AGCTGGCAGGCGGTTTTCGAAAGTCAAGTGTGAAATCCCGGGCTCAACCTGGGAACGG 600
Qy 624 CATTGAGACTGCAAGACTAGAGTGTGAGGGGGGTAGAAATCCGCGTGTAGCAGTG 683
Db 601 CATTGAGACTGCAAGACTGAGGTTTGGCAGAGGGGGGTGAAATTCACGTTGAGCAGTG 660
Qy 684 AAATGCGTAGAGATGCGGAGGAATAACGATGGCGAAGGACGCCCTCGGATGACACTGA 743
Db 661 AAATGCGTAGAGATGCGGAGGAATAACGATGGCGAAGGACGCCCTCGGATGACACTGA 720
Qy 744 CGCTCATGCAAGAGCGTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCGCT 803
Db 721 CGCTCATGCAAGAGCGTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCGCT 780
Qy 804 AAACGATGTCATAGTCTGTTGGGGTTTGAATCC--TTGGTAGCGTAGCTTAACGCGTGA 861
Db 781 AAACGATGTCATAGTCTGTTGGGGTTTGAATCC--TTGGTAGCGTAGCTTAACGCGTGA 840
Qy 862 AATTGACCGCTGGGAGTACGCGCGCAAGGTTAAAACTCAAAAGGAATTGACGGGACCC 921
Db 841 AGTTGACCGCTGGGAGTACGCGCGCAAGGTTAAAACTCAAAAGGAATTGACGGGACCC 900
Qy 922 GCACAAGCGTGGATGATGGAATTAATTGATGCAACGCGAAGAAACCTTACCTGCTCTT 981
Db 901 GCACAAGCGTGGATGATGGAATTAATTGATGCAACGCGAAGAAACCTTACCTGCTCTT 960
Qy 982 GACATGTACGGAATCTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGGTG 1041
Db 961 GACATGTACGGAATCTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGGTG 1020
Qy 1042 CTGCATGCTGTCTGTCAGCTCGTGTCTGAGATGCTTGGGTTAAGTCCCGCAACGAGCGCA 1101
Db 1021 CTGCATGCTGTCTGTCAGCTCGTGTCTGAGATGCTTGGGTTAAGTCCCGCAACGAGCGCA 1080
Qy 1102 ACCCTTGTCAATTAGTTCCTCATTTTGTGGGCACTCTTAATGAGATGTCGGGTGACAAA 1161
Db 1081 ACCCTTGTCAATTAGTTCCTCATTTTGTGGGCACTCTTAATGAGATGTCGGGTGACAAA 1140
Qy 1162 CCGGAGGAAGTGGGGATGACGTCAGTCTCATGGCCCTTATGAGCAGGCGCTTTCACACG 1221
Db 1141 CCGGAGGAAGTGGGGATGACGTCAGTCTCATGGCCCTTATGAGGATGGGCTTTCACACG 1200
Qy 1222 TCATACAAATGGTTCGCTACAGAGGGTCCGTAAGCCGCGAGGTGGTGCCTAATCTCATAAAC 1281
Db 1201 TCATACAAATGGTTCGCTACAGAGGGTTCGTAAGCCGCGAGGGGAGGCCAAATCTCAGAAGC 1260
Qy 1282 CGATCGTAGTCCGGATCGCACTCTTGCAACTCGAGTGTGAAAGTGTGGAATCGCTAGTAAT 1341
Db 1261 CGATCGTAGTCCGGATCGCACTCTTGCAACTCGAGTGTGAAAGTGTGGAATCGCTAGTAAT 1320
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Qy 1342 CCAGATCAGATCTGCGTGAATAGTTCCGGGTCTTTGATACACACCGCCCGTCAAC 1401
Db 1321 CGCGATCAGATCGCGGTGAATACGTTCCCGGTCTTTGATACACACCGCCCGTCAAC 1380
Qy 1402 CATGGAGTCAAGTTTACCAAGAGTGGTAGCTAACCG 1440
Db 1381 CATGGAGCGGGTCTGCCAAGAGTAGTTAGCCTAACCG 1419

RESULT 5
US-10-029-397A-38
; Sequence 38, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI-076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Bordetella bronchiseptica
US-10-029-397A-38

Query Match 80.7%; Score 1161.6; DB 7; Length 1532;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 1273; Conservative 1; Mismatches 161; Indels 5; Gaps 1;

Qy 1 TGAGAGTTTGATCTCGGCTCAGATTGAACGCTGGGGCATGCTTTACACATCAAGTCG 60
Db 6 TGAGAGTTTGATCTCGGCTCAGATTGAACGCTGGGGCATGCTTTACACATCAAGTCG 65
Qy 61 AACGGTAACAGGTGCTTGACCGCTGACAGTGGCGAAACGGGTAGTAAATGCGTCGAA 120
Db 66 GACGGCAGCACGGGCTTCGGCTGCTGGCGAGTGGCGAAACGGGTAGTAAATGTCGAA 125
Qy 121 TGTAACGTGTAATGGGGATAGCTCGCGAAGCCGATTAATACCGCATACGCCCTGAG 180
Db 126 CGTGCCCACTAGCGGGGGTAATCTACGCGAAGCGTGGCTTAATACCGCATACGCCCTAG 185
Qy 181 GGGGAAGCGGGGATCGAAGACCTCGCGTTATACGAGCAGCGCGTCTGATTAGCTA 240
Db 186 GGGGAAGCGGGGACCTTCGGGCTTCGCACTATTGAGCGCGCGGATATCGAATTAGCTA 245
Qy 241 GTTGGTGAAGTAAGAGCTCAACGAGCGACGATCAGTAGCGGTCTGAGAGGATGATCCG 300
Db 246 GTTGGTGGGTAAACGGCTTACCAAGCGACGATCCGTAGCTGTTGAGAGGACGACCA 305
Qy 301 CCACACTGGAGCTGAGACACCGGCCAGACTCTTACGGGAGGACGAGTGGGGAATTTGG 360
Db 306 CCACACTGGAGCTGAGACACCGGCCAGACTCTTACGGGAGGACGAGTGGGGAATTTGG 365
Qy 361 ACAATGGGGCAACCTGTATCCAGCCATGCGCGTGTCTGAAGAAGCCCTTCGGGTGTA 420
Db 366 ACAATGGGGCAACCTGTATCCAGCCATCCCGGTGTGCGATGAAGCCCTTCGGGTGTA 425
Qy 421 AAGGACTTTTGTGAGGAGGAAATCCCGTGGTTAATACCCGCGGGGATGACAGTACCB 480
Db 426 AAGCACTTTTGGCAGGAAAGAAACGGCAGCGGTAAATATCTGTGCAACTGACGGTACCT 485
Qy 481 GAAGAATAAGCAGCGCTAAGTGTGCGAGCGCCGCGTAAATAGTAGGGTGAAGCG 540
Db 486 GCAGAATAAGCAGCGCTAAGTGTGCGAGCGCCGCGTAAATAGTAGGGTGAAGCG 545
Qy 541 TTAATCGGAATTACTGGCGCTAAAGCGTGGCAGGCGGTTTTCGAAGTCTGTGTAAG 600
Db 546 TTAATCGGAATTACTGGCGCTAAAGCGTGGCAGGCGGTTTTCGAAGAAAGATGTGAAT 605
Qy 601 CCCCGGGCTCAACCTGGGAAACGGCATTTGGAGACTGCAAGACTAGAGTGGCTCAGAGGGG 660

Db 606 CCAGGCTTAACCTTGGAACTGCAATTTTAACTACCGGCTAGAGTGTGTACAGGGAG 665
Qy 661 GTAGATTCGCGGTGAGCAGTGAATGCGTAGAGATCGGAGGAATACCGATGGCGAAG 720
Db 666 GTGGAATTCGCGGTGAGCAGTGAATGCGTAGATATCGGAGGAACACCGATGGCGAAG 725
Qy 721 GCAGCCCCCTGGGATGACACTGACGCTATGACAGAAAGCGTGGGAGCAACAGGATTA 780
Db 726 GCAGCCCTCTGGGATAACACTGACGCTCATGACAGAAAGCGTGGGAGCAACAGGATTA 785
Qy 781 GATACCTCGTAGTCCACGCCCTTAAACGATGTCATAGCTGTGGGGGTTTGAATCCTT 840
Db 786 GATACCTCGTAGTCCACGCCCTTAAACGATGTCATAGCTGTGGGGGCTTCCGGGCTT 845
Qy 841 GGTAGCGTAGCTAAACGCGTGAATTTGACCGCCTGGGAGTACGCGCAAGGTTTAAACT 900
Db 846 GGTAGCGTAGCTAAACGCGTGAATTTGACCGCCTGGGAGTACGCGCAAGGTTTAAACT 905
Qy 901 CAAAGGAATTGACGGGACCCGACAAAGCGGTGGATGATGTGATTAATTCGATGCAACG 960
Db 906 CAAAGGAATTGACGGGACCCGACAAAGCGGTGGATGATGTGATTAATTCGATGCAACG 965
Qy 961 CGAAAAACCTTACCTGCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGGCCGA 1020
Db 966 CGAAAAACCTTACCTGCTCTTGACATGTCTGGAATCCCGAAGAGATTTGGGAGTGTCTGC 1025
Qy 1021 AAGGAGCGGTAAACACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1026 AAGAGAACCGGAACACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
Qy 1081 TTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCTCATTTAGTTGGGCACTCT 1140
Db 1086 TTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCTACGAA- - - - -GGGCACTCT 1140
Qy 1141 AATGAGCTGCGGTGACAAAACGGAGGAAGGTGGGATGACGCTCAAGTCTCTATGSCCC 1200
Db 1141 AATGAGCTGCGGTGACAAAACGGAGGAAGGTGGGATGACGCTCAAGTCTCTATGSCCC 1200
Qy 1201 TTATGAGCAGGCTTCCACACGTCATCAATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1201 TTATGAGTGGGCTTCCACACGTCATCAATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Qy 1261 GTGGTCCCAATCTCATAAACCGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGCT 1320
Db 1261 GGGAGCCATCCAGAAACCGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGCT 1320
Qy 1321 GAAGTCGGAATCGTAGTAATCGAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCT 1380
Db 1321 GAAGTCGGAATCGTAGTAATCGAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCT 1380
Qy 1381 TGTACACACCGCCCGTCACACCATGGAGTGGTTTCCACAGAGTGGGTAGGCTAACCG 1440
Db 1381 TGTACACACCGCCCGTCACACCATGGAGTGGTTTCCACAGAGTGGGTAGGCTAACCG 1440

RESULT 6
US-10-168-337A-4
; Sequence 4, Application US/10168337A
; Publication No. US20030170654A1
; GENERAL INFORMATION:
; APPLICANT: Crocetti, Gregory R.; Tyson, Gene W.; Hugenholtz, Philip; and Blackall,
; APPLICANT: Linda L.
; TITLE OF INVENTION: Probes and Primers for the Detection of Polyphosphate
; FILE REFERENCE: 002367PC/KF
; CURRENT APPLICATION NUMBER: US/10/168,337A
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1460
; TYPE: DNA


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QY 262 CAAGGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCGCCACACACTGGGACTGAGACACG 321
Db 241 CAAGGCGACGATCAGTAGCTGCTGAGAGGACGACCCAGCCACACTGGGACTGAGACACG 300
QY 322 GCCGAGACTCTTACCGGAGGAGCAGAGTGGGAAATTTTGGACAATGGGGGCAACCTTGATC 381
Db 301 GCCCAGACTCTTACCGGAGGAGCAGAGTGGGAAATTTTGGACAATGGGGGCAACCTGATC 360
QY 382 CAGCATGCCCGTGTCTGAAGAAGGCTTCGSGTTCTGAAGGACTTTTCTCAGGGAGGA 441
Db 361 CAGCAATGCCCGTGTGTGAAGAAGGCTTCGSGTTCTGAAGGACTTTTCTCAGGAAGA 420
QY 442 AATCCCGCTGTTAATACCCGGGGGATGACAGTACCBGAAGAATAAGCACCGGCTTAAC 501
Db 421 AATCATTTCTGGCTAATACCCGGAGTGATGACGTACCGGAAGAATAAGCACCGGCTAAC 480
QY 502 TAGTGCACAGCCCGGTTAATACGTAGGTCGACGCTTAATCGGAATTAATCTGGCGT 561
Db 481 TAGTGCACAGCCCGGTTAATACGTAGGTCGACGCTTAATCGGAATTAATCTGGCGT 540
QY 562 AAAGCGTCCGAGCGGTTTGCAGTCTGATGTGAAGCCCGGGCTCAACCTGGGAAC 621
Db 541 AAAGCGTCCGAGCGGTTTGCAGTCTGATGTGAAGCCCGGGCTCAACCTGGGAAC 600
QY 622 GGCAATTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGGGTGAAGATTTCCGCGTGTAGCAG 681
Db 601 TGCATTGTGACTGGCAGGCTAGAGTATGCGAGAGGGGGTGAAGATTTCCAGCTGTAGCAG 660
QY 682 TGAATTCGCTAGAGATCGGAGGAATAACGATGCGAAGCAGCGCCCTGGGATGACACT 741
Db 661 TGAATTCGCTAGAGATGCGAGGAATAACGATGCGAAGCAGCGCCCTGGGCAATACT 720
QY 742 GACGCTCATCGAAGCGTGGGAGCAACAGGATTAGATACCCCTGGTAGTCCACGCC 801
Db 721 GACGCTCATCGAAGCGTGGGAGCAACAGGATTAGATACCCCTGGTAGTCCACGCC 780
QY 802 CTAAACGATGCTCAATTAGCTGTTGGGGTTTGAATCCTTGCTAGCGTAGCTAAACGGGTGA 861
Db 781 CTAAACGATGCTCAATTAGCTGTTGGGGTTTCAATTCCTTAGTAACTAGCTAAACGGGTGA 840
QY 862 AATTGACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAAGGAATTGACGGGACCC 921
Db 841 AGTTGACCGCTGGGAGTACGCGTCGCAAGATTAATACTCAAAAGGAATTGACGGGACCC 900
QY 922 GCACAAGCGTGGATGATGTGGATTAATTCGATGCAACGCGAAGAACTTACCTGCTCTT 981
Db 901 GCACAAGCGTGGATGATGTGGATTAATTCGATGCAACGCGAAGAACTTACCTGCTCTT 960
QY 982 GACATGTACGGAACCTTGGTAGAGATATCTTGGTGCCCGAAGGGAGCCGTAACACAGGTG 1041
Db 961 GACATGTGCGAAGCCCGATGAGAGTTGGCGTGCTCGAAGAGAACCCGCGCACAGGTG 1020
QY 1042 CTGCATGGCTGTGCTGACGCTGCTGTGAGATGTTGGGTTAAGTCCCGCAACGACGCGCA 1101
Db 1021 CTGCATGGCTGTGCTGACGCTGCTGTGAGATGTTGGGTTAAGTCCCGCAACGACGCGCA 1080
QY 1102 ACCCTTGTCAATTAGTTGCCATCATTTAGTTGGGCACTCTAATCAGACTGCGGTTGACAA 1161
Db 1081 ACCCTTGTCTTGTAGTTGCTACGCAAG - - - - -GCACCTTAAGGAGACTGCGGTTGACAA 1135
QY 1162 CCGGAGGAAGGTGGGATGACGTCAAGTCTCATGGCCCTTATGAGCAGGGCTTTCACAG 1221
Db 1136 CCGGAGGAAGGTGGGATGACGTCAAGTCTCATGGCCCTTATGAGGAGGGCTTTCACAG 1195
QY 1222 TCATACATGGCTGCTGACAGAGGTGCTTAAGCCGCGAGAGGTGTGCCAATCTCATTAAC 1281
Db 1196 TCATACATGGCTGCGAACAGAGAGGTGCGCAACCCGCGAGGGGAGGCAATCCGAGAAAC 1255
QY 1282 CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGCATGGAAGTTCGGAATTCGCTAGT 1341
Db 1256 CGATCGTAGTCCGATCTGCAACTCGAGTGCATGGAAGTTCGGAATTCGCTAGT 1315
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QY 1342 CGCAGATCAGCATCTGCGTGAATACGTTCCGGGCTTGTGTACACACCGCCCGTACAC 1401
Db 1316 CGCGGATCAGCATGCGCGGTGAATACGTTCCGGGCTTGTGTACACACCGCCCGTACAC 1375
QY 1402 CATGGAGTGAAGTTTACCAGAAAGTGGGTAGGCTAACCG 1440
Db 1376 CATGGAGTGGGTTTTTACCAGAAAGTGGGTAGGCTAACCG 1414

RESULT 8
US-10-168-337A-2
; Sequence 2, Application US/10168337A
; Publication No. US20030170654A1
; GENERAL INFORMATION:
; APPLICANT: Crocetti, Gregory R.; Tyson, Gene W.; Hugenholtz, Philip; and Blackall,
; APPLICANT: Linda L.
; TITLE OF INVENTION: Probes and Primers for the Detection of Polyphosphate
; FILE REFERENCE: 002367PC/KF
; CURRENT APPLICATION NUMBER: US/10/168,337A
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Rhodocyclus tenuis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 50..59
; OTHER INFORMATION: n = unknown
US-10-168-337A-2
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Query Match 80.5%; Score 1159; DB 7; Length 1460;
Best Local Similarity 88.9%; Pred. No. 0;
Matches 1262; Conservative 1; Mismatches 154; Indels 2; Gaps 1;
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QY 24 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTGCAGCGGTAAACAGGGTCTTGACC 83
Db 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTGCAGCGGTAAACAGGGTCTTGACC 60
QY 84 GTGACGAGTGGCGAAGCGGTGAGTAAATGCTGCGGAATGTACCGTGTAAATGGGGGATAGC 143
Db 61 GCGCAGAGTGGCGAAGCGGTGAGTAAATGCTGCGGAATGTACCGTGTAAATGGGGGATAGC 120
QY 144 TCGGCGAAGCGGATTAATACCGCATACGCTGAGGGGGAAGCGGGGATCGAAGA 203
Db 121 GTAGCGAAGTTACGCTAATACCGCATATTCGTGTAGCAGGAAGCAGGGGATCTTAGGA 180
QY 204 CTTGCGGTTTATACGACGAGCCGACGCTCTGATTAGCTTAGTTGGTGAAGTAAAGCTCACCA 263
Db 181 CTTGCGGTTTGGGAGCGCCGATGTCGGATTAGCTTAGTTGGTGAAGTAAAGCTCACCA 240
QY 264 AGCGACGATACGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 323
Db 241 AGCGACGATACGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 300
QY 324 CCAGACTCTACGGGAGGAGCAGTGGGAAATTTTGGACAATGGGGGCAACCCGTATCCA 383
Db 301 CCAGACTCTACGGGAGGAGCAGTGGGAAATTTTGGACAATGGGGGCAACCCGTATCCA 360
QY 384 GCCATGCCCGTGTCTGAAGAAGGCGCTTCGGGTTGTAAAGAGCTTTTGTTCAGGGAGGAAA 443
Db 361 GCCATGCCCGTGTGAGTGAAGAAGGCGCTTCGGGTTGTAAAGCTTTTTCGGGGGAGGAAA 420
QY 444 TCCCGCTGTTTAATACCCCGGGGAGTACAGTACCBGAAGAATAAGCACCGGCTAACTA 503
Db 421 TGCGACTGGCTAATACCTGCTGATGACGGTACCGGAAGAAAGAACACCGGCTAACTA 480
QY 504 CGTGCCAGCAGCCGGGTAAATACGTAGGTCGCAAGCGTTAATCGGAATTTACTGGGGCTAA 563
Db 481 CGTGCCAGCAGCCGGGTAAATACGTAGGTCGCAAGCGTTAATCGGAATTTACTGGGGCTAA 540
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Qy 564 AGCTGCGCAGCGGTTTGCAGCTCTGATGTGAAGCCCGCGGCTCAACCTGGAAACGG 623
Db |||||
Qy 541 AGCGTGCAGCGCGGTTGTGTAAGACAGAGCTGAAATCCCGCGGCTCAACCTGGAACTG 600
Db |||||
Qy 624 CATTGGAGAGCTGCAAGACTAGAGTCGCTCAGAGGGGGGTAGAATTCGCGGTGTAGCAGTG 683
Db |||||
Qy 601 CGTTTGTGACTGACAGCTAGAGTTTGGCAGAGGGGGTGGAAATTCACGCTGTAGCAGTG 660
Db |||||
Qy 684 AAATGCTAGAGATGCGGAGGAATACCGATGCGGGAAGCGAGCCCGCTGGGATGACACTGA 743
Db |||||
Qy 661 AAATGCTAGAGATGTGGAGGAACACCGATGGCGAAGCGAGCCCGCTGGGCAATACTGA 720
Db |||||
Qy 744 CGCTCATGCAAGAAAGCGTGGGAGCAACAGGAATTAGATACCCCTGTAGTCCACGCGCT 803
Db |||||
Qy 721 CGCTCATGCAAGAAAGCGTGGGAGCAACAGGAATTAGATACCCCTGTAGTCCACGCGCT 780
Db |||||
Qy 804 AAACGATGTCAATTAGCTGTGG--GGGGTTTGAATCTTGGTAGCGTAGCTAAACGCGTGA 861
Db |||||
Qy 781 AAACGATGTCAACTAGGTGTGGTGGGTAAACCCATTAGTGCCTGTAGCTAAACGCGTGA 840
Db |||||
Qy 862 AATTGACCGCTGGGAGTACGGCCGCAAGGTTAAACTCTAAGGAATTGAGCGGGACCC 921
Db |||||
Qy 841 AGTTGACCGCTGGGAGTACGGCCGCAAGGTTAAACTCTAAGGAATTGAGCGGGACCC 900
Db |||||
Qy 922 GCACAAGCGGTGATGTGGATTAAATTCGATGCAACGCGAATAAACCCTTACCTGCTCTT 981
Db |||||
Qy 901 GCAACAAGCGGTGATGTGGATTAAATTCGATGCAACGCGAATAAACCCTTACCTGCTCTT 960
Db |||||
Qy 982 GACATGTACGGAACCTTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAACACAGGTG 1041
Db |||||
Qy 961 GACATGTACGGAACCTTGGTAGAGATATGGGAGTCCCGAAGGGAACCTGAAACACAGGTG 1020
Db |||||
Qy 1042 CTGCATGGCTGCTGCTAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1101
Db |||||
Qy 1021 CTGCATGGCTGCTGCTAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1080
Db |||||
Qy 1102 ACCCTGTGCTAGTGTGCATCATTTAGTTGGGCACTCTAATGAGACTGCCGGTGCACAA 1161
Db |||||
Qy 1081 ACCCTGTGCTAATTTGCCATCATTTAGTTGGGCACTCTAATGAGACTGCCGGTGCACAA 1140
Db |||||
Qy 1162 CCGGAGGAAGTGGGGATGAGCTCAAGTCTCATGGCCCTTATGAGCAGGCTTCACACG 1221
Db |||||
Qy 1141 CCGGAGGAAGTGGGGATGAGCTCAAGTCTCATGGCCCTTATGGTAGGGCTTCACACG 1200
Db |||||
Qy 1222 TCATACAAATGTCGGTACAGAGGTGCTTAGCGCGAGGTTGGTGGCCATCTCATAAAC 1281
Db |||||
Qy 1201 TCATACAAATGTCGGTCCAGAGGTTGCCAACCCGCGAGGGGAGCCAATCCCGCAAGC 1260
Db |||||
Qy 1282 CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCTAGTAAT 1341
Db |||||
Qy 1261 CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCTAGTAAT 1320
Db |||||
Qy 1342 CGCAGATCAGCATGTCGGTGAATACGTTCCCGGCTTGTACACACCCCGCTGCACAC 1401
Db |||||
Qy 1321 CGCGGATCAGCATGTCGGGTTGAATACGTTCCCGGCTTGTACACACCCCGCTGCACAC 1380
Db |||||
Qy 1402 CATGGAGTAGTTTACACAGAGTGGGTAGGCTAAACCG 1440
Db |||||
Qy 1381 CATGGAGCGGGTTCTGCGAAGTAGTTAGCCTTAACCG 1419
Db |||||
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RESULT 9
US-10-029-397A-45
; Sequence 45, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029.397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73

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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 1544  
; TYPE: DNA  
; ORGANISM: Neisseria meningitidis  
US-10-029-397A-45  
  
Query Match 80.5%; Score 1159; DB 7; Length 1544;  
Best Local Similarity 89.1%; Pred. No. 0;  
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;  
  
Qy 4 AGAGTTTGTAGTCTCGGCTCAGATTGAACGCTGGGGCATGCTTTACACATCAAGTCSAAC 63  
Db |||||  
Qy 9 AGAGTTTGTAGTCTCGGCTCAGATTGAACGCTGGGGCATGCTTTACACATCAAGTCSAAC 68  
Db |||||  
Qy 64 GGTA-----ACAGGTGCTTGCACCGCTGACGAGTGGCGAAACGGGTGAGTAATGCGTCG 117  
Db |||||  
Qy 69 GGCAGCACACAGAGAAGCTTGTCTTCGGGTGGCGAGTGGCGAAACGGGTGAGTAACATATCG 128  
Db |||||  
Qy 118 GAATGTACCGTGAATGGGGGATAGCTCGCGGAAAGCCGATTAATAACCCATACGCGCT 177  
Db |||||  
Qy 129 GAACGTACCCAGTAGTGGGGATAACTGATCGAAGATCAGCTAATAACCCGATACGCTT 188  
Db |||||  
Qy 178 GAGGGGAAAGCGGGGATCGAAAGACCTCGCGTTATACGAGCAGCCGACGTCTGATTAG 237  
Db |||||  
Qy 189 GAGAGAGAAAGCAGGGGACCTTCGGGCTTTCGCTATTCGAGCGCGCATATCTGATTAG 248  
Db |||||  
Qy 238 CTAGTTGGTGAAGTAGAGCTCAACAAAGGCGAGTACAGTAGCGGGTCTGAGAGGATGAT 297  
Db |||||  
Qy 249 CTAGTTGGTGGGTAAAGGCTTACAAAGGCGAGTACAGTAGCGGGTCTGAGAGGATGAT 308  
Db |||||  
Qy 298 CCGCCACACTGGAGCTGAGACACGGCCAGACTCTACGGGAGGCGACAGTGGGGAAATTT 357  
Db |||||  
Qy 309 CCGCCACACTGGAGCTGAGACACGGCCAGACTCTACGGGAGGCGACAGTGGGGAAATTT 368  
Db |||||  
Qy 358 TGACAAATGGGGGCAACCTTGATCCAGCCATGCGCGTGTCTGAAGAAGCGCTTCGGGTT 417  
Db |||||  
Qy 369 TGGACAAATGGCGCAAGCCGTGATCCAGCCATGCGCGTGTCTGAAGAAGCGCTTCGGGTT 428  
Db |||||  
Qy 418 GTAAAGGACTTTTGTGAGGAGGAAATCCGCTGGTTAATACCCGGCGGGGATGACAGTA 477  
Db |||||  
Qy 429 GTAAAGGACTTTTGTGAGGAGGAAAGGCTGTGCTAATATACAGCGGCTGATACCGTA 488  
Db |||||  
Qy 478 CCBGAACAATAAGCACCGGCTAACTAGCTGCCAGCAGCCGGTAAATACGTAGGGTGCAG 537  
Db |||||  
Qy 489 CTTGAAGATATAGCACCGGCTAACTAGCTGCCAGCAGCCGGTAAATACGTAGGGTGCAG 548  
Db |||||  
Qy 538 GCGTTAAATCGGAAATTAATCTGGGCGTAAAGCGTGGCGAGCGGTTTTCGAAGTCTCATGTA 597  
Db |||||  
Qy 549 GCGTTAAATCGGAAATTAATCTGGGCGTAAAGCGGCGCAGACGCTTACTTTAAGCAGGATGTA 608  
Db |||||  
Qy 598 AAGCCCCGGGCTCAACCTGGGAACGGCAATTGGAGACTTGCAGACTAGAGTGCCTCAGAGG 657  
Db |||||  
Qy 609 AATCCCCGGGCTCAACCCGGGAACTGCGTTCTGAACCTGGGTGACTCGAGTGTGCAGAGG 668  
Db |||||  
Qy 658 GGGGTAGAAATTCGCGGTGTAGCAGTGAATTCGCTAGAGATGCGGAGGAATACCGATGGCG 717  
Db |||||  
Qy 669 GAGGTAGAAATTCAGGTGTAGCAGTGAATTCGCTAGAGATGTGGAGGAATACCGATGGCG 728  
Db |||||  
Qy 718 AAGGCAGCCCCCTGGGATGACACTGACGCTCATGCACGAAGCGTGGGGAGCAACAGGA 777  
Db |||||  
Qy 729 AAGGCAGCCCTCTGGGACAACTGACGTTTATGCCCGGAAGCGTGGGTGAGCAACAGGA 788  
Db |||||  
Qy 778 TTAGATACCTGGTGTAGTCCAGCCCTAAACGATGCTAATAGCTGTTGGG--GGTTCGAAT 836  
Db |||||  
Qy 789 TTAGATACCTGGTGTAGTCCAGCCCTAAACGATGCTAATAGCTGTTGGGCAACCTGATT 848  
Db |||||  
Qy 837 CTTGGTAGCGTAGCTAAACGCGTGAATTTGACCCCTGGGGAGTACGCGCCCAAGGTTAA 896  
Db |||||  
Qy 849 GCTTGGTAGCGTAGCTAAACGCGTGAATTTGACCCCTGGGGAGTACGCTCGCAAGATTAA 908  
Db |||||  
Qy 897 AACTCAAAGGAATTTGACGGGGACCCGCAAGCGGTGATGATGTGATTAATTCGATCG 956  
Db |||||
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Db 909 AACTCAAAGGAATTGACGGGGACCCGACAAAGCGGTGGATGATGTGGATTAATTCGATGC 968
Qy 957 AACCGGAAAACCTTACCTGCTCTTTGACATGTACGGAACTTGGTAGAGATATCTTGTGC 1016
Db 969 AACCGGAAGAACCTTACTGCTCTTGACATGTACGGAA--TCCTCCGGAGACGGAGAGT 1026
Qy 1017 CCGAAAAGGAGCCGTAACACAGAGTGCTGCATGGCTGCTGACGCTCGTGTGAGATGT 1076
Db 1027 GCCTTCGGGAGCCGTAACACAGAGTGCTGCATGGCTGCTGACGCTCGTGTGAGATGT 1086
Qy 1077 TGGGTTAAGTCCCGCAAGCGGCAACCTTGTCTATTAGTGGCATCAATTAGTTGGGCA 1136
Db 1087 TGGGTTAAGTCCCGCAAGCGGCAACCTTGTCTATTAGTGGCATCAATTAGTTGGGCA 1146
Qy 1137 CTCTAATGAGACTCCCGGTGACAAACCGGAGGAAGTGGGGATGACGCTCAAGTCCCTCATG 1196
Db 1147 CTCTAATGAGACTCCCGGTGACAAACCGGAGGAAGTGGGGATGACGCTCAAGTCCCTCATG 1206
Qy 1197 GCCCTTATGACGGGCTTCAACGTCATCAATGGTTCGGTACAGAGGGTTCGCTAAGCCG 1256
Db 1207 GCCCTTATGACGGGCTTCAACGTCATCAATGGTTCGGTACAGAGGGTTCGCTAAGCCG 1266
Qy 1257 CGAGTGGTCCCATCTCATAAACCGCATCGTAGTCCGGATCGCACTCTGCAACTCGAGT 1316
Db 1267 CGAGTGGTCCCATCTCATAAACCGCATCGTAGTCCGGATCGCACTCTGCAACTCGAGT 1326
Qy 1317 GCGTGAAGTCGGAATCGTAGTAAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGG 1376
Db 1327 GCATGAAGTCGGAATCGTAGTAAATCGCAGTCAAGCATCTGCGGTGAATACGTTCCCGG 1386
Qy 1377 GTCTTGATACACCGCCCGTCAACCATGGAGTGAGTTTCAACAGAAAGTGGGTAGGCTA 1436
Db 1387 GTCTTGATACACCGCCCGTCAACCATGGAGTGAGTTTCAACAGAAAGTGGGTAGGATA 1446
Qy 1437 ACC 1439
Db 1447 ACC 1449

RESULT 10
US-10-915-740A-1068
; Sequence 1068, Application US/10915740A
; Publication No. US20050191316A1
; GENERAL INFORMATION:
; APPLICANT: Frazer, Claire M.
; APPLICANT: Hickey, Erin
; APPLICANT: Peterson, Jeremy
; APPLICANT: Tettelin, Herve
; APPLICANT: Venter, J. Craig
; APPLICANT: Maignani, Vega
; APPLICANT: Galeotti, Cesira
; APPLICANT: Mora, Manroza
; APPLICANT: Ratti, Giulio
; APPLICANT: Scarselli, Maria
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
; FILE REFERENCE: 002441.00090
; CURRENT APPLICATION NUMBER: US/10/915,740A
; PRIORITY FILING DATE: 2004-08-11
; PRIORITY FILING DATE: 09/806,866
; PRIORITY FILING DATE: 1999-10-08
; PRIORITY FILING DATE: USSN 60/103,794
; PRIORITY FILING DATE: 1998-10-09
; PRIORITY FILING DATE: USSN 60/132,068
; PRIORITY FILING DATE: 1999-04-30
; PRIORITY FILING DATE: PCT/US99/25373
; NUMBER OF SEQ ID NOS: 1068
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1068

; LENGTH: 2242716
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-915-740A-1068
Query Match 80.5%; Score 1159; DB 10; Length 2242716;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;
Qy 4 AGAGTTTGATCTCGGCTCAGAGCTGAAGCTGGCGGATGCTTTACACATCGAAGTCGAAC 63
Db 307723 AGAGTTTGATCTCGGCTCAGAGCTGAAGCTGGCGGATGCTTTACACATCGAAGTCGAAC 307782
Qy 64 GGTG-----ACAGGGTGGCTTGACCGCTGACAGGTGGCGAAGCGGGTGAAGTAAATGCGCTG 117
Db 307783 GGCAGCACAGAGAAGCTTCTTCTCGGTGGCGAGTGGCGAAGCGGGTGAAGTAAATGCGCTG 307842
Qy 118 GAATGTACCGTGTAAATGGGGATAGCTCGCGGAAAGCGGATTAATACCCGATACGCCCT 177
Db 307843 GAACGTACCGAGTAGTGGGGATAAAGTGAATGAGTAAATACAGCTAAATACCGATACGCTCT 307902
Qy 178 GAGGGGAAGCGGGGATCGAAGACCTCGCTTATACAGCAGCGGATGCTGATGATG 237
Db 307903 GAGAGAGAAGCAGGGGACCTTCGGGCTTTCGCTATTCGAGCGGCGATATCTGATGATG 307962
Qy 238 CTAGTTGGTGAAGTAAGAGCTCAACCAAGGCGACGATCAGTAGCGGGTCTCGAGAGGATGAT 297
Db 307963 CTAGTTGGTGGGTAAAGGCTTACCAAGGCGACGATCAGTAGCGGGTCTCGAGAGGATGAT 308022
Qy 298 CCGCCACACTGGGACTGAGACACGCGCCAGACTCTTACCGGAGGCGAGCAGTGGGGAAATTT 357
Db 308023 CCGCCACACTGGGACTGAGACACGCGCCAGACTCTTACCGGAGGCGAGCAGTGGGGAAATTT 308082
Qy 358 TGACAAATGGGCGCAAGCCCTGATCCAGCCATGCGCGGTCTCTGAAGAAGCCCTTCGGGTT 417
Db 308083 TGACAAATGGGCGCAAGCCCTGATCCAGCCATGCGCGGTCTCTGAAGAAGCCCTTCGGGTT 308142
Qy 418 GTAAAGGACTTTTGTGAGGGAGGAAATCCCGCTGGTTAATACCCGCGGGGATGACAGTA 477
Db 308143 GTAAAGGACTTTTGTGAGGGAGGAAAGGCTGTGTCTAATATCAGCGGCTGATGACGGTA 308202
Qy 478 CCBGAAGAATAAGCACCGGCTAACTAGTGCACAGCAGCGCGGTAATACTAGGGTGCAA 537
Db 308203 CCGTGAAGAATAAGCACCGGCTAACTAGTGCACAGCAGCGCGGTAATACTAGGGTGCAA 308262
Qy 538 GCGTTAATCGGAATTACTGGGCTGAAGCGTGCAGCGGCGTTTTCGAAGTCTGATGTA 597
Db 308263 GCGTTAATCGGAATTACTGGGCTGAAGCGTGCAGCGGCGTTTTCGAAGTCTGATGTA 308322
Qy 598 AAGCCCGGGCTCAACCTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGG 657
Db 308323 AATCCCGGGCTCAACCTGGGAACCTGGTTCTGAACTGGGTGACTCGAGTGTCTCAGAGG 308382
Qy 658 GGGGTAGAAATTCGCGTGTAGCAGTGAATAGCTAGAGATGCGGAGAGTAATACCGATGGCG 717
Db 308383 GAGGTAGAAATTCACCGTGTAGCAGTGAATAGCTAGAGATGCGGAGAGTAATACCGATGGCG 308442
Qy 718 AAGGACGCCCCCTGGGATGACACTGACGCTGATGCAAGCGTGGGAGGCAACAGGA 777
Db 308443 AAGGACGCCCCCTGGGATGACACTGACGCTGATGCAAGCGTGGGAGGCAACAGGA 308502
Qy 778 TTAGATACCTCTGTAGTCCACGCGCTTAAACGATGTCAATAGCTGTGGG--GGTTTGAAT 836
Db 308503 TTAGATACCTCTGTAGTCCACGCGCTTAAACGATGTCAATAGCTGTGGGCAACCTGATT 308562
Qy 837 CTTTGTAGCGGTAGCTAAACGCGTGAATTTGACCGCTCGGGAGTACCGCCGCAAGGTTAA 896
Db 308563 GCTTGTAGCGGTAGCTAAACGCGTGAATTTGACCGCTCGGGAGTACCGCTCGCAAGATTAA 308622
Qy 897 AACTCAAGGAATTGACGGGGACCCGCAAGCGGTGGATGATGTCGATTAATTCGATGC 956
Db 308623 AACTCAAGGAATTGACGGGGACCCGCAAGCGGTGGATGATGTCGATTAATTCGATGC 308682

Db	1699862	AACGCGAAGAACCTTACCTCGTCTTGACATGTACGGAA--TCCTCCGGAGACAGGAGAGT	1699905
Qy	1017	CCGAAAGGGAGCCGTAAACACAGAGTGTCTGATGGCTGTCGTGAGTCTCGTGTGAGATGT	1076
Db	1699804	GCCTTCGGGAGCCGTAAACACAGGTGCTGATGGCTGTCGTGAGTCTCGTGTGAGATGT	1699845
Qy	1077	TGGGTTAAGTCCCGCAACGAGCGCAACCCCTGTGATTTAGTTGGCA	1136
Db	1699844	TGGGTTAAGTCCCGCAACGAGCGCAACCCCTGTGATTTAGTTGGCA	1699785
Qy	1137	CTCTAATGAGACTGCCGGTGACAAACGGAGGAGGTGGGGATGACGTCAAGTCTCATG	1196
Db	1699784	CTCTAATGAGACTGCCGGTGACAAACGGAGGAGGTGGGGATGACGTCAAGTCTCATG	1699725
Qy	1197	GCCCTTATGAGCAGGGCTTCACACGTCAATATGGTTCGGTACAGAGGGTTCGCTAAGCCG	1256
Db	1699724	GCCCTTATGAGCAGGGCTTCACACGTCAATATGGTTCGGTACAGAGGGTTCGCTAAGCCG	1699665
Qy	1257	CGAGGTGGTCCCAATCTCAATAAACCGATCGTAGTCCGGATTCGCACACTCGAGT	1316
Db	1699664	CGAGGTGGTCCCAATCTCAATAAACCGATCGTAGTCCGGATTCGCACACTCGAGT	1699605
Qy	1317	GCCTGAAGTCGGATCGCTAGTAAATCCGACATCAGCATGCTGCGTGAATACGTTCCCGG	1376
Db	1699604	GCATGAAGTCGGATCGCTAGTAAATCCGAGGTGAGCATATCTGCGGTGAATACGTTCCCGG	1699545
Qy	1377	GTCTTGTACACACCGCCGTCACACATGGAGTGAGTTCACACAGAGTGGGTAGGCTA	1436
Db	1699544	GTCTTGTACACACCGCCGTCACACATGGAGTGGGGATACCAAGTAGTAGATA	1699485
Qy	1437	ACC 1439	
Db	1699484	ACC 1699482	
RESULT 12			
US-10-168-337A-1			
; Sequence 1, Application US/10168337A			
; Publication No. US20030170654A1			
; GENERAL INFORMATION:			
; APPLICANT: Crocetti, Gregory R.; Tyson, Gene W.; Hugenholtz, Philip; and Blackall,			
; APPLICANT: Linda L.			
; TITLE OF INVENTION: Probes and Primers for the Detection of Polyphosphate			
; TITLE OF INVENTION: Accumulating Organisms in Wastewater			
; FILE REFERENCE: 002367PC/KF			
; CURRENT APPLICATION NUMBER: US/10/168,337A			
; CURRENT FILING DATE: 2000-12-27			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 1460			
; TYPE: DNA			
; ORGANISM: Rhodocyclus tenuis			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: 50, 59, 881			
; OTHER INFORMATION: n = unknown, m = a or c			
US-10-168-337A-1			
Query Match 80.4%; Score 1157.6; DB 7; Length 1460;			
Best Local Similarity 88.8%; Pred. No. 0;			
Matches 1260; Conservative 2; Mismatches 155; Indels 2; Gaps 1;			
Qy	24	ATTGAACGCTGGGGCATGCTTTACACATCGAAGTCGAACGGTAAACAGGGTGTTCGACC	83
Db	1	ATTGAACGCTGGGGCATGCTTTACACATCGAAGTCGAACGGTAAACAGGGTGTTCGACC	60
Qy	84	GCTGACGAGTGGCGAACCAGGTGAGTAATGCGTCCGAATGACCGTGAATGGGGGATAGC	143
Db	61	GGCGACGAGTGGCGAACCAGGTGAGTAATGCAATCGGAACGTGCCCTGNAAGTGGGGATAC	120
Qy	144	TCGGCGAACCAGGTAAATACCGCATACGCCCTGAGGGGGAAAGCGGGGATCGAAGA	203

Db	121	GTAGCGAAAGTTACGCTAATAACCGCATATTTCTGTGACAGGAAGCAGGGGATCTTAGGA	180
Qy	204	CCTCGGTTTATACGACGACGCGACGCTCTGATTAGCTAGTTGGTGAAGTCAAGCTCACCA	263
Db	181	CCTTCGGCTTTGGGACGCGCGATGTCGGATTAGCTAGTTGGTGAAGTCAAGCTCACCA	240
Qy	264	AGCGACGATCAGTAGCGGCTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC	323
Db	241	AGCGACGATCAGTAGCGGCTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC	300
Qy	324	CCGACTCCCTACGGGAGGACGAGTGGGAAATTTTGGCAATATGGGGCAACCTGTATCCA	383
Db	301	CCGACTCCCTACGGGAGGACGAGTGGGAAATTTTGGCAATATGGGGCAACCTGTATCCA	360
Qy	384	GCATGCCGCTGCTCTGAAGAAGGCTTCGGGTGTAAAGGACTTTTGTTCAGGGAGGAAA	443
Db	361	GCATGCCGCTGAGTGAAGAAGGCTTCGGGTGTAAAGGCTTTTTCGGGGGGAAGAAA	420
Qy	444	TCCCGCTGTTAATACCCCGCGGGGATGACAGTACCBGAAGAATAAGCACCGGCTAACTA	503
Db	421	TGGMACTGGCTAATACCTGCTGATGACCGGTACCCGAAGAAGAACACCGGCTAACTA	480
Qy	504	CGTGCCAGCAGCGCGCTTAATAGTAGGGTGCAAGCGTTAATCGGAATTAATCGGGCTAA	563
Db	481	CGTGCCAGCAGCGCGCTTAATAGTAGGGTGCAAGCGTTAATCGGAATTAATCGGGCTAA	540
Qy	564	AGCGTCGCGAGGCGGTTTTGCAAGTCTGATGTGAAAGCCCGGGCTCAACCTGGGAACGG	623
Db	541	AGCGTCGCGAGGCGGTTTTGTAAGACAGACGTGAATATCCCGGGCTCAACCTGGGAAC	600
Qy	624	CAATTGGAGACTGCAAGACTAGAGTCGTGAGAGGGGGTAGAATTCGCGTGTAGCAGTG	683
Db	601	CGTTTGTGACTGACACAGCTAGAGTTTGGCAGAGGGGGTGAATTCACCGTGTAGCAGTG	660
Qy	684	AAATGCTAGAGATGCGGAGGAATACCGATGGCGAAGGCGAGCCCTCGGATGACACTGA	743
Db	661	AAATGCTAGAGATGCGGAGGAATACCGATGGCGAAGGCGAGCCCTCGGATGACACTGA	720
Qy	744	CGCTCATGCACGAAACGCTGGGAGCAACAGAGTTAGATACCTGCTAGTCCACGCGCT	803
Db	721	CGCTCATGCACGAAACGCTGGGAGCAACAGAGTTAGATACCTGCTAGTCCACGCGCT	780
Qy	804	AAACGATGTCAATTAGCTGTG--GGGGTTTGAATCCTTGGTAGCGTGTAGTAAACGCTGA	861
Db	781	AAACGATGTCAATTAGCTGTG--GGGGTTTGAATCCTTGGTAGCGTGTAGTAAACGCTGA	840
Qy	862	AATTGACCGCTGGGAGTACGCGCCGAGGTTTAAACTCAAGGAAATTCAGCGGGACCC	921
Db	841	AGTTGACCGCTGGGAGTACGCGCCGAGGTTTAAACTCAAGGAAATTCAGCGGGACCC	900
Qy	922	GCACAAAGCGTGGATGATGTGGATTAAATTCGATGCAACGCGGAAACCTTTACCTGCTTT	981
Db	901	GCACAAAGCGTGGATGATGTGGATTAAATTCGATGCAACGCGGAAACCTTTACCTGCTTT	960
Qy	982	GACATGTACGGAACCTTGGTAGAGATATCTTGGTCCCGGAAAGGAGCGCTTAACACAGGTG	1041
Db	961	GACATGTACGGAACCTTGGTAGAGATATCTTGGTCCCGGAAAGGAGCGCTTAACACAGGTG	1020
Qy	1042	CTGCATGGCTGTGCTGACGTGCTGAGATGTTGGGTAAAGTCCCGCAACAGGCGCA	1101
Db	1021	CTGCATGGCTGTGCTGACGTGCTGAGATGTTGGGTAAAGTCCCGCAACAGGCGCA	1080
Qy	1102	ACCTTGTCTATTAGTTGCCATCAATTTAGTTGGGCACTCTAATCAGACTGCGGCTGACAA	1161
Db	1081	ACCTTGTCTATTAGTTGCCATCAATTTAGTTGGGCACTCTAATCAGACTGCGGCTGACAA	1140
Qy	1162	CCGAGGAAGGTGGGATGACCTCAAGTCTCATGCGCCCTTATGAGCAGGGCTTCACAG	1221
Db	1141	CCGAGGAAGGTGGGATGACCTCAAGTCTCATGCGCCCTTATGAGTGGGTAGGGCTTCACAG	1200
Qy	1222	TCATACATGGTGGTACAGAGGTGCTTAAGCCGCGAGGTGGTGGCAATCTCATAAAC	1281
Db	1201	TCATACATGGTGGTCCAGAGGTTGCCAACCCCGGAGGGGAGGCAATCCCGCAAGC	1260

Qy 1282 CGATCTAGTCCGATCGCACTCTGCAACTCGAGTCCGTGAGTCGGAATCGCTAGTAAT 1341
Db 1261 CGATCGTAGTCCGGAATGCACTGCAACTCGACTCGATGAAGTCGGAATCGCTAGTAAT 1320
Qy 1342 CGCAGATCAGCATGCTCGGGTGAATAGTTCCTCCGGGTCTTGTACACACCGCCCGTCACAC 1401
Db 1321 CGCGGATCAGCATGCTCGGGTGAATAGTTCCTCCGGGTCTTGTACACACCGCCCGTCACAC 1380
Qy 1402 CATGGGAGTGAGTTTACCAGAAAGTGGGTAGGCTAAACCG 1440
Db 1381 CATGGAGGGGTTCTGCGCAAGTAGTGTAGCCTAAACCG 1419

RESULT 13
US-09-726-774-5
; Sequence 5, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L. Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoea
US-09-726-774-5

Query Match 80.0%; Score 1152; DB 3; Length 1544;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1282; Conservative 1; Mismatches 152; Indels 9; Gaps 3;

Qy 4 AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGATGCTTTACATGCAATGCGAAC 63
Db 9 AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGATGCTTTACATGCAATGCGAAC 68
Qy 64 GGTAAAC-----AGGTCCTTGCACCGCTGACGAGTGGCGAACGGGTGAGTAATGCGTCG 117
Db 69 GGCAGCACAGGAAAGCTTGTCTCGGTGGAGTGGCGAACGGGTGAGTAATGCGTCG 128
Qy 118 GAATGTATCCGTGTAATGGGGATAGCTCGGCGAAAGCCGGATTAAATACCGCATACGCCCT 177
Db 129 GAACGTACCGGTAGCGGGGATTAATCTGATCGAAAGATCAGCTAATACCGCATACGCTT 188
Qy 178 GAGGGGAAAGCGGGGATCGAAAGACTCGCGTTATACGAGCAGCGCATCTGTATGATAG 237
Db 189 GAGAGGAAAGCAGGGGACCTTCGGGCTTCGGCTATCCGAGCGCCGATATCTGATTAAG 248
Qy 238 CTAGTTGTGAGTGAAGGCTCACAGGCGCAAGCTAGTACGGGTCTGAGAGGATCAT 297
Db 249 CTGGTTGGCGGGTAAAGGCCACCAAGGCGACCATAGTACGGGTCTGAGAGGATGAT 308
Qy 298 CCGCCACTCTGGGACTGAGACACGCGCCAGACTCTTACGGGAGGCGAGCTGGGGAAATT 357
Db 309 CCGCCACTCTGGGACTGAGACACGCGCCAGACTCTTACGGGAGGCGAGCTGGGGAAATT 368
Qy 358 TGGCAATATGGGGCAACCTGATCAGCCATGCGCGTGTCTGAAGAGGCTTCGGGTT 417
Db 369 TGGCAATATGGGGCAACCTGATCAGCCATGCGCGTGTCTGAAGAGGCTTCGGGTT 428
Qy 418 GTAAGGACTTTTGTACGGAGGAATCCCGTGTGTAATACCGCGGGGATGACAGTA 477
Db 429 GTAAAGGACTTTTGTACGGAGGAATAGGCTGTGCGCAATATCGCGGCCGATGACGGTA 488
Qy 478 CCBGAAGAATAAGCACCGGCTAACTACGTGCGCAGCGCGGTAATACGTAGGCTGCAA 537

Db 489 CCTGAAGAAATAAGCAACGGCTAACTAGTGCACAGACCGCGGTAATAACGTAGGGTGCGA 548
Qy 538 GCCTTAATCGGAATTAAGCGCTAAAGCGTGCAGCGCGGTTTTCGAAGTCTCTGATGTA 597
Db 549 GCCTTAATCGGAATTAAGCGCGTAAAGCGGGCGCAGACGGTACTTTAAGACAGATGTA 608
Qy 598 AAGCCCGGGCTCAACTCGGGAACGGCATTTGGAGATGTCGAAGACTAGAGTGCCTGACAGG 657
Db 609 AATCCCGGGCTCAACCCGGGAACCTGGTTCGAACTGGGTGACTCGAGTGTGTACAGG 668
Qy 658 GGGGTAGAAATTCGCGGTGTAGCAGTGAATGCTGTAGAGATGCGGAGGAATACCGATGGCG 717
Db 669 GAGGTGGAATTTCCACGTGTAGCAGTGAATGCTGTAGAGATGTCGAGGAATACCGATGGCG 728
Qy 718 AAGGCAGCCCCCTGGGATGACACTGACCTCATGCAGAAAGCGTGGGAGCAACAGGA 777
Db 729 AAGGCAGCCCCCTGGGATTAACCTGACGTTTTCGAAAGCGTGGGTAGCAACAGGA 788
Qy 778 TTAGATACCCCTGGTAGTCCACGCGCTAAACGATGTCAATTAGCTGTGGG-GGTTTGAAT 836
Db 789 TTAGATACCCCTGGTAGTCCACGCGCTAAACGATGTCAATTAGCTGTGGGCAACTTGATT 848
Qy 837 CCTTGGTAGCTAGCTAAACCGCTGAAATTGACCGCTGGGAGTACGCGCGCAAGGTAA 896
Db 849 GCTTGGTAGCTAGCTAAACCGCTGAAATTGACCGCTGGGAGTACGCGTCCCAAGATTAA 908
Qy 897 AACTCAAGGAATTGACGGGACCGCACAGCGGTGGATGTGGAATTAATTCGATGC 956
Db 909 AACTCAAGGAATTGACGGGACCGCACAGCGGTGGATGTGGAATTAATTCGATGC 968
Qy 957 AAGCGGAAAAACCTTACCTCTTGTACATGTACGGAACCTTGGTAGAGATATCTTGGTGC 1016
Db 969 AAGCGGAAAGAACCTTACCTCTTGTGACATGTGCGGAA--TCCTCCGAGACGAGGAGT 1026
Qy 1017 CCGAAAGGGAGCCGTAAACAGAGTGTGATGCTGTGTCAGTCTGTGTCGTGAGATGT 1076
Db 1027 GCCTTCGGGAGCGGTAAACAGAGTGTGATGCTGTGTCGTGTCGTGTCGTGAGATGT 1086
Qy 1077 TGGGTTAAGTCCCGCAACGAGCGCAACCTTGTTCATTAGTTGCCATCATTTAGTTGGGCA 1136
Db 1087 TGGGTTAAGTCCCGCAACGAGCGCAACCTTGTTCATTAGTTGCCATCATTTCCGTTGGGCA 1146
Qy 1137 CTCTAATGAGACTGCCGTCACAAACCGGAGGAGGTGGGATGACGTCAGTCTCTCATG 1196
Db 1147 CTCTAATGAGACTGCCGTCACAAACCGGAGGAGGTGGGATGACGTCAGTCTCTCATG 1206
Qy 1197 GCCTTTATGAGCAGGGCTTCAACGCTCATACATGCTGCTGCTGTAAGAGGTCGTTAAGCCG 1256
Db 1207 GCCTTTATGAGCAGGGCTTCAACGCTCATACATGCTGCTGCTGTAAGAGGTCGTTAAGCCG 1266
Qy 1257 CGAGGTGTCGCAATCTCATAAACCGATCGTAGTCCGGATCGCAGTCTGCACTCGCACTCGAGT 1316
Db 1267 CGAGGTGTCGCAATCTCATAAACCGATCGTAGTCCGGATTCGACTCTGCACTCGAGT 1326
Qy 1317 CGGTGAAGTCGGAATCCCTAGTAAATCGCAGATCAGCATGCTCGGTCGGAATACGTTCCCGG 1376
Db 1327 GCATGAAGTCGGAATCCCTAGTAAATCGCAGTCAAGTCTGCGTGAATACGTTCCCGG 1386
Qy 1377 GTCTTTACACACCGCCGTCACACCATGGAGTGAATTCACACAGAAAGTGGGTAGGCTA 1436
Db 1387 GTCTTTACACACCGCCCGTCAACCATGGAGTGGGGATACCAAGAAAGTAGGTAGGCTA 1446
Qy 1437 ACCG 1440
Db 1447 ACCG 1450

RESULT 14
US-10-029-397A-44
; Sequence 44, Application US/10029397A
; Publication No. US2003015709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.

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; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMB1:076US
; CURRENT APPLICATION NUMBER: US/10/029.397A
; PRIORITY FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 44
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-029-397A-44

Query Match      80.0%; Score 1152; DB 7; Length 1544;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1282; Conservative 1; Mismatches 152; Indels 9; Gaps 3;

QY 4 AGAGTTTGATCTCGCTCAGATTGAACCGCTGGCGGATGCTTTACATGCAAGTCAAGC 63
DB 9 AGAGTTTGATCTCGCTCAGATTGAACCGCTGGCGGATGCTTTACATGCAAGTCAAGC 68
QY 64 GGTAAAC-----AGGCTGCTTGCACCGCTGACGAGTGGCGAAGCGGTGAGTAATGCGTCG 117
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QY 118 GAATGTACCGGTGTAATGGGGATAGCTCGGCGAAGCGCGGATTAAATACCGCATACGCGCT 177
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QY 178 GAGGGGAAACCGGGGATCGAAGACCTCGGCTTATACGAGCGCGAGCTCTGATTAG 237
DB 189 GAGAGGAAACGAGCGGACCTTCGGGCTTTGCGCTATCCGAGCGCGCGATATCTGATTAG 248
QY 238 CTAGTTGCTGAGTAAGAGCTCACAAAGGCGACCATCAGTAGCGGGTCTGAGAGGATGAT 297
DB 249 CTGTTGGCGGGTAAAGGCCCAACAAAGCGACCATCAGTAGCGGGTCTGAGAGGATGAT 308
QY 298 CCGCCACACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGCGACAGTGGGGAATTT 357
DB 309 CCGCCACACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGCGACAGTGGGGAATTT 368
QY 358 TGGCAATAGGGGCAACCGCTGATCAGCGCATGCGCGGTGCTGAAAGAGCGCTTCGGGTT 417
DB 369 TGGCAATAGGGGCGAAGCGCTGATCAGCGCATGCGCGGTGCTGAAAGAGCGCTTCGGGTT 428
QY 418 GTAAGGACTTTTCTCAGGGAGGAATCCGCTGTTTAAATACCGCGCGGGATGACAGTA 477
DB 429 GTAAGGACTTTTCTCAGGGAGGAATCCGCTGTTTAAATACCGCGCGGGATGACAGTA 488
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DB 489 CCBGAAGAATAAGCACCGGCTTAACCTGTCGACGACCGCGGTAATACGTAGGGTGCGA 548
QY 538 CGGTTAATCGGAATTAATCGGCTGTAAGCGTGCAGCGCGGTTTTCGAAGTCTGATGTA 597
DB 549 CGGTTAATCGGAATTAATCGGCTGTAAGCGTGCAGCGCGGTTTTCGAAGTCTGATGTA 608
QY 598 AAGCCCCGGGCTCAACTCTGGGAACCGCATGGAGCTGCAAGACTAGAGTGCCTCAGAGG 657
DB 609 AATCCCCGGGCTCAACTCTGGGAACCGCATGGAGCTGCAAGACTAGAGTGCCTCAGAGG 668
QY 658 GGGGTAGAAATTCGCGGTGTAAGCAATCGGTGAGAGTGGCGGGAATACCGCATGGCG 717
DB 669 GAGGTGAAATTCACCGTGTAGCAGTGAATCGGTGAGAGTGGCGGGAATACCGCATGGCG 728
QY 718 AAGCAGCCCCCTGGGATGATCATGACGCTCATGCAAGAAAGCGTGGGAGCAACAGGA 777
DB 729 AAGCAGCCCCCTGGGATGATCATGACGCTCATGCAAGAAAGCGTGGGAGCAACAGGA 788
QY 778 TTAGATACCCCTGGTGGTTCACGCGCTTAAACGATGCTCAATAGCTGTTGGG-GGTTTGAAT 836
DB 789 TTAGATACCCCTGGTGGTTCACGCGCTTAAACGATGCTCAATAGCTGTTGGGCAACTTGAT 848
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QY 897 AACTCAAGGAATTTGACGGGGACCCGCAACGCGGTGGATGATGTGGATTAATTCGATGC 956
DB 909 AACTCAAGGAATTTGACGGGGACCCGCAACGCGGTGGATGATGTGGATTAATTCGATGC 968
QY 957 AACGCGAAAAACCTTACTCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGC 1016
DB 969 AACGCGAAGAACCTTACTCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGC 1026
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DB 1387 GTCTTTGACACACCGCGCTACACCATGAGGAGTGTTCACAGAGTGGGTAGGCTA 1446
QY 1437 ACCG 1440
DB 1447 ACCG 1450

RESULT 15
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; Sequence 5, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; PRIORITY FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-719-633-5

Query Match      80.0%; Score 1152; DB 8; Length 1544;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1282; Conservative 1; Mismatches 152; Indels 9; Gaps 3;

QY 4 AGAGTTTGATCTCGCTCAGATTGAACCGCTGGCGGATGCTTTACATGCAAGTCAAGC 63
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Db 9 AGAGTTTGTATCTGGCTCAGATTGAACGCTGGCGCATGCTTTACATGCAAGTCGGAC 68
Qy 64 GGTAAAC-----AGGTCCTTGCACCGCTGACGAGTGGCGAAACGGGTGAGTAATGCGTCG 117
Db 69 GGCAGCACAGGAAGCTTGTCTTCGGGTGGCGAGTGGCGNAACGGGTGAGTACATATCG 128
Qy 118 GAATGTACCGGTGTAATGGGGATAGCTCGCGGAAAGCCGGATTAATACCGGATACGCCCT 177
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Qy 358 TGGCAATGGGGGCAACCTGATCCAGCCATGCCGCTGTCTGAAGAGGCCCTTCGGGTT 417
Db 369 TGGCAATGGGGGCAAGCCTGATCCAGCCATGCCGCTGTCTGAAGAGGCCCTTCGGGTT 428
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Db 429 GTAAAGGACTTTTGTACGGAGGAAAGAGGCTGTTGCCAATATCGCGGCCGATGACGGTA 488
Qy 478 CCBGAAGAAATGAACACCGGCTAACTACGTGCCAGAGCCCGGGTAAATACGTAGGGTGCAA 537
Db 489 CCTGAAGAAATGAACACCGGCTAACTACGTGCCAGAGCCCGGGTAAATACGTAGGGTGCGA 548
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Qy 658 GGGGTAGAAATCCCGGTGTAGCAGTGAATTCGGTGAAGATCGGAGGAAATACCGATGGCG 717
Db 669 GAGGTGAATTCACGCTAGCAGTGAATTCGGTGAAGATGAGAGTGGAGGAATACCGATGGCG 728
Qy 718 AAGCAGCCCTCTGGGATGACACTGACGCTCATGCAAGCGTGGGAGCAACACAGGA 777
Db 729 AAGGAGCCCTCTGGGATGAACACTGACGTTCAITGCCAAGCGTGGGTAGCAACACAGGA 788
Qy 778 TTAGATACCTGGTAGTCCACGCCCTAAACCGATGTCAATTAGCTGTTGGG-GGTTTGAAT 836
Db 789 TTAGATACCTGGTAGTCCACGCCCTAAACCGATGTCAATTAGCTGTTGGGCAACTTGATT 848
Qy 837 CTTTGGTAGCTAGCTAACCGGTGAATTTGACCGCTTGGGAGTACGGCCGCAAGGTTAA 896
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Qy 1437 ACCG 1440
Db 1447 ACCG 1450

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Job time : 1998 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 02:07:20 ; Search time 27 Seconds
(without alignments)
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Title: US-10-678-023A-1

Perfect score: 1439.2

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA New:*

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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029.4	71.5	1531	7	US-11-256-221-1
2	221.2	15.4	5849	7	US-11-270-287-1
3	125.4	8.7	1799	7	US-11-217-529-195588
4	125.4	8.7	1799	7	US-11-217-529-195589
5	125.4	8.7	1799	7	US-11-217-529-195590
6	125.4	8.7	1799	7	US-11-217-529-195591
7	125.4	8.7	1799	7	US-11-217-529-195592
8	119.8	8.3	1773	7	US-11-256-428-61
9	103.2	7.2	22118	7	US-11-284-877-16
10	103	7.2	1869	6	US-10-511-937-333
11	91	6.3	42999	7	US-11-284-877-17
12	40	2.8	600	7	US-11-217-529-166170
13	40	2.8	600	7	US-11-217-529-166173
14	39.4	2.7	954	6	US-10-488-619-1
15	35	2.4	883	7	US-11-256-428-46
16	35	2.4	883	7	US-11-256-428-64
17	32.8	2.3	3228	6	US-10-342-836-47
18	28.8	2.0	378	7	US-11-284-877-22
19	28.6	2.0	2747	6	US-10-196-749-101
20	28.4	2.0	381	7	US-11-217-529-166773
21	28.4	2.0	795	7	US-11-217-529-190902
22	28	1.9	378	7	US-11-284-877-21
23	28	1.9	1389	7	US-11-217-529-78881
24	27.4	1.9	984	7	US-11-217-529-327
25	27.2	1.9	822	7	US-11-217-529-174437

ALIGNMENTS

RESULT 1

US-11-256-221-1

; Sequence 1, Application US/11256221

; Publication No. US20060094094A1

; GENERAL INFORMATION:

; APPLICANT: Sugio, Tsuyoshi

; APPLICANT: Miura, Akira

; APPLICANT: Parada Valdecantos, Pilar A.

; APPLICANT: Badilla Ohlbaum, Ricardo

; TITLE OF INVENTION: BACTERIA STRAIN WENELEN DSM 16786, USE OF SAID BACTERIA FOR

; TITLE OF INVENTION: LEACHING OF ORES OR CONCENTRATES CONTAINING METALLIC SULFIDE

; TITLE OF INVENTION: MINERAL SPECIES AND LEACHING PROCESSES BASED ON THE USE OF SAID

; TITLE OF INVENTION: BACTERIA OR MIXTURES THAT CONTAIN SAID BACTERIA

; FILE REFERENCE: 15053.15US01

; CURRENT APPLICATION NUMBER: US/11/256, 221

; CURRENT FILING DATE: 2005-10-21

; PRIOR APPLICATION NUMBER: CL 2731-2004

; PRIOR FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 1531

; TYPE: DNA

; ORGANISM: Bacteria

US-11-256-221-1

Query Match 71.5%; Score 1029.4; DB 7; Length 1531;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 1203; Conservative 1; Mismatches 233; Indels 4; Gaps 3;

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Db 1 TGAGAGTTTGATCTCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCG 60

Qy 61 AACGGTAACAGGCTGCTTGACCGCTGACGAGTGGCGAAACGGGTGAGTAAATGCGTCGGAA 120

Db 61 AACGGTAACAGG--TCTTCGATGCTGACGAGTGGCGGCGGCGGTGAGTAAATGCGTAGGAA 118

Qy 121 TGTACCTGTATGGGGGATAGCTCGCGGNAACCGGATTAATACCGCATACGCCCTGAG 180

Db 119 TCTGTCTTTTGTAGTGGGGGACAAACCCAGGAAATCTGGGCTTAATACCGCATACGCCCTGAG 178

Qy 181 GGGGAAAGCGGGGATCGAAAGACCTCGCTTATACGAGCGCGGACGCTCTGATTAGCTA 240

Db 179 GGGGAAAGCGGGGATCTTCGGACCTTCGCGCTAAGAGAGGAGGCTAGTCCGATTAGCTA 238

Qy 241 GTTGGTGAGGTAAGAGCTCAACCAAGCGGACGATCAGTAGCGGCTCTGAGAGGATGATCCG 300

Db 241 GTTGGTGAGGTAAGAGCTCAACCAAGCGGACGATCAGTAGCGGCTCTGAGAGGATGATCCG 300

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Db 241 GTTGGTGAGGTAAGAGCTCAACCAAGCGGACGATCAGTAGCGGCTCTGAGAGGATGATCCG 300

Db 239 GTTGGCGGGTAAAGGCCCAACAAAGGCGACGATCGGTAGCTGTGCTGAGAGGACGACCAG 298
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Qy 361 ACAATGGGGGCAACCTGATCAGGCATGCGCGTGTCTGAAGAAGGCTTCGGGTTGTA 420
Db 359 GCAATGGGGGCAACCTGACGAAGCAATGCCGCTGGATGAAGAAGGCTTCGGGTTGTA 418
Qy 421 AAGGACTTTTGTGAGGAGGAATCCCGCTGGTTAAATACCCCGCGGGGATGACAGTACCB 480
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Qy 481 GAAGAATAAGCACCGGCTAACTACGTCCACGACGCGCGTAAATACGTAGGGTCCAAAGCG 540
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Db 599 CCCCGGCTCAACTGGGAAATGGCGTGGAAACCGGTGTACTAGATGATGGAGGGTG 658
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RESULT 2

US-11-270-287-1
; Sequence 1, Application US/11270287
; Publication No. US20060099627A1
; GENERAL INFORMATION:
; APPLICANT: Kara, Anna K.
; APPLICANT: Ting, Robert C.
; APPLICANT: Tham, Jill M.
; APPLICANT: Nelson, James S.
; APPLICANT: Tan, Theresa M.
; TITLE OF INVENTION: Diagnosis of Parasites
; FILE REFERENCE: 64-99
; CURRENT APPLICATION NUMBER: US/11/270,287
; CURRENT FILING DATE: 2005-11-09
; PRIOR APPLICATION NUMBER: US/09/369,992
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: PCT/IB98/00212
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: AU P09481/97
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: AU P09329/97
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: AU P04953/97
; PRIOR FILING DATE: 1997-02-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5849
; TYPE: DNA
; ORGANISM: Plasmodium berghel
US-11-270-287-1

Query Match 15.4%; Score 221.2; DB 7; Length 5849;
Best Local Similarity 54.8%; Pred. No. 1.4e-64;
Matches 645; Conservative 0; Mismatches 468; Indels 63; Gaps 8;

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Db 4474 AAGAAATGTACAATCACATTAGGGATTGAAATAAAGCCCTAAATTTTTTTAAATCAGCAG 4533
Qy 348 TGGGGAATTTTGGACAATGGGGCAACCTGATCCAGCCATCGCCGCTGTCTGAAGAAGG 407
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Db 4594 TATATTTTATATTTGTAACCTTTATA-----TTTTATTTTAAAT 4633
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Db 4634 ATTGATAAAAAATAAAACAATTAGTATTGCTTAATTTCTGTCCAGCAGCGCGTAAATA 4693
Qy 528 TAGGTGCAACCGTTTAATTCGGAAATTAAGCGGTAAAGCGTCCGAGCGGTTTTCGAAG 587
Db 4694 GAAATAACACCGTTTATTC-ACCTTTATTTGGGTAAAGCGTTTTTAAGGTTTTATATTAAT 4752
Qy 588 TCTGATGGAAGCCCGCGGCTCAACCTGGGAAACGGCATTTGGAGACTCAAGACTAGAGT 647
Db 4753 TTTATTTTAAAAATATTTAAATTTAAATTTGAAATAAAAAATAAATAATAATAAGAGT 4812

Qy	648	CGGTCAGAGGGGGTAGAAATCCCGGTGTAGCAGTGAATTCGTPAGAGATCGCGAGGAAT	707
Db	4813	ATTATAAAGGATTAAAGAAATTTTGTGAGAAGTAGTGAATGCAATGATGATCAAAAAAGAAT	4872
Qy	708	ACCGATGGCAAGGCAGCCCTCGGTGATGACACTGACGCTCATGCGACGAAGCGTGGGA	767
Db	4873	ACCAAGGCGAAGGCATAACTATATAATAAATGACACTTATAACGAAGCTAAGGTA	4932
Qy	768	GCAAAACAGGATATAGATACCTGTGTGATGCCACGCCCTAAACGATGTCAATTAGCTGTGGG	827
Db	4933	GCAAAATAGGATTAGATACCTCTAGTAGTCTTAGCTGTAAACTATGAATATATTTATATTTAT	4992
Qy	828	GGTTTGAATCCTTGGTAGCGTAGCTAACGCGTGAATTTGACCGCTGGGAGGTACGCGCG	887
Db	4993	ATAATT--AATATAAATATAATACTAAGTAATAATAATTCGCGCTGAGTAGTATATTCG	5050
Qy	888	CAAGGTTAAAACTCAAAGGAATTGACGGGGACCCGCAACAAGCGGTGGATGATGTGGATTA	947
Db	5051	CAAGAACGAAATTCAAAGGAATTCGACGGGAGCTTATACAAGTGTGGAAACATGTGGCTTA	5110
Qy	948	ATTCGATGCAACGGGAAACCTTACCTGCTCTTGACATGTACGGAACTTGGTAGAGATA	1007
Db	5111	ATTGATGCAACACGATAAACCTTACCAAAATTTAACTAATTTTATTTAATAAGGAAT	5170
Qy	1008	TCCTGGTCCGGAAGGGAGCGGTAAACACAGGTGCTGCATGGTGTGTCAGCTCGTGTC	1067
Db	5171	ANTAGTTTAATANA-----TATATAGTAGTCATGGCTGTGTCAGTTCGTCTGTCT	5221
Qy	1068	GTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTTGTCAATTAGTTGCCATCATTT	1127
Db	5222	GTGAAGTATTAAATTTAAGTATTATAACGAACGTAAACCTTTTATAAAAAATTTTAT	5281
Qy	1128	AGTTGGGCACTCTAATGAGACTCGCGGTGACAAACGGAGAGGTGGGGAATGACGTCAA	1187
Db	5282	AATATATTTTATAAT-----ATATAAAAAAGACTACGTCAA	5318
Qy	1188	GTCTCATGCGCCTTATGAGCAGGGCTTCACAGTCAACAATGGTCGGTACAGAGGTC	1247
Db	5319	GTCAATTATGCTCCTTATTTTGGCTGCTCACGTGTACATAAATATAACAAATTTT	5378
Qy	1248	GCTAAGCCGGAGGTGTGGCAATCTCATAAAAACCGATCGTAGTCCGGATCGCACTCTGC	1307
Db	5379	ATTA-----TATGAAATATAATATTAATAATATTTATAGTCTCTGATTATAAATGA	5432
Qy	1308	AACTCGAGTGGTGAAGTCGGAATCGCTAGTAAATCGCAGATCAGCA--TGCTCGGCTGAAT	1366
Db	5433	AACTCATTATATGAAGATGGAAATCACTAGTAATCGCTAATAAAGATGATAGCGGTAAT	5492
Qy	1367	ACGTTCCCGGTCCTGTACACACGCCGCGTCACACC	1402
Db	5493	AAGTTCTTAAGCTTTGTACACACGCCGCGTCACATC	5528

Qy	1277	AA AAC -CGATCGTAGTCCGGATCCGACTCTGCAACTCGATGCGTGAAGTCGGAATCGCT	1335
Db	1522	GAAACTCCGTCGCTGGGATAGACATTGTAATTATTCCTCTTCAACGAGGAATTCCT	1581
Qy	1336	AGTAATCGCAGATCAGCATGCTCGGTGTAATAGTTCCCGGGTCTTGTCACACCGCCCG	1395
Db	1582	AGTAAGGCCAAGTCATCAGCTTCGGTTGATTAGTCCCTGCCCTTTGTACACACCGCCCG	1641
Qy	1396	TCACACCATGGGAGTGAGT	1414
Db	1642	TCGCTAGTACCGATTGAAT	1660

RESULT 4
US-11-217-529-195589
; Sequence 195589, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED

```
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195589
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195589

Query Match      8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;

QY 649 CGTCAGAGGGGGTAGAATCCGCGGTAGCAGTCAAAATCGTAGAGATCGGAGGAATA 708
DB 869 CGGTGGGGGATCAGTATCAATTTGTGAGAGGTGAATTTCTGGATTTATTGAAGACTA 928

QY 709 CCGATGGCGAAGGAGCGCCCTCGGATGACACTGACGCTCATGCACGAAAGCGTGGGGAG 768
DB 929 ACTACTGCGAAGCATTTGCCAAGACGTTTTCATTAATCAAGAACGAAAGTAGGGGAT 988

QY 769 CAACAGAGATTAGATACCTCGTGTAGTCCAGCCCTTAAACGATGTCATTAAGTCTGTGGG 828
DB 989 CGAAGATGATCAGATACCGTGTAGTCTTAAACCATAACTATGCCGACTAGGATCGGGT 1048

QY 829 GTTTGAATCCTTGGTAGGTAGTCAACGCGTGAATTCGACCGCT-----G 874
DB 1049 GGTGTTTTTTAATGACCCACTCGGCACCTTACGAGAAATCAAGTCTTTGGGTTCTGGG 1108

QY 875 GGGAGTACGGCGCAAGGTTAAACTCAAGGAATTTGACGG--GGACCGCAACAGCGGTG 933
DB 1109 GGGAGTATGTCGCAAGGCTGAACCTTAAAGGAATTTGACGGAAGGGCACCAGGAGTG 1168

QY 934 GATGATGTGGATTAAATTCGATGCAACGGGAAACCTTACCTGCTCTTGACATGTACGGA 993
DB 1169 GAGCCTGGCGCTTAAATTTGACTCAACACGGGGAATCTCACCAGGTCCAGACA-----C 1221

QY 994 ACTTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGAGTCTGCATGGCTGT 1053
DB 1222 AATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGGTGGTGGTGCATGGCCGT 1281

QY 1054 CGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCT----- 1106
DB 1282 TCTTAGTTGGTGGAGTATTTGCTGCTTAAATTCGATAACGAAACGAGACCTTAACCTAC 1341

QY 1107 TGTCAATAGTTGCCATCAATTTAGT-----TGGGCACTCTAATGACACTGCCGCTGACAAA 1161
DB 1342 TAAATAGTGGGTAGCAATTTGCTGGTATCCACTCTTTAGAGGACATATCGTTTCAAG 1401

QY 1336 AGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCTTGTACACACCGCCCG 1395
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DB 1582 AGTAAGCGCAAGTCATCAGCTTGGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCG 1641
QY 1396 TCACACCATGGGAGTGAGT 1414
DB 1642 TCGCTAGTACCGATTGAAT 1660

RESULT 5
US-11-217-529-195590
; Sequence 195590, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195590
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195590

Query Match      8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;

QY 649 CGTCAGAGGGGGTAGAATTCGCGGTAGCAGTGAATTCGAGATCGGAGGAATA 708
DB 869 CGGTGGGGGATCAGTATCAATTTGTGAGAGGTGAATTTCTGGATTTATTGAAGACTA 928

QY 709 CCGATGGCGAAGGAGCGCCCTCGGATGACACTGACGCTCATGCACGAAAGCGTGGGGAG 768
DB 929 ACTACTGCGAAGCATTTGCCAAGACGTTTTCATTAATCAAGAACGAAAGTAGGGGAT 988

QY 769 CAACAGAGATTAGATACCTCGTGTAGTCCAGCCCTTAAACGATGTCATTAAGTCTGTGGG 828
DB 989 CGAAGATGATCAGATACCGTGTAGTCTTAAACCATAACTATGCCGACTAGGATCGGGT 1048

QY 829 GTTTGAATCCTTGGTAGGTAGTCAACGCGTGAATTCGACCGCT-----G 874
DB 1049 GGTGTTTTTTAATGACCCACTCGGCACCTTACGAGAAATCAAGTCTTTGGGTTCTGGG 1108

QY 875 GGGAGTACGGCGCAAGGTTAAACTCAAGGAATTTGACGG--GGACCGCAACAGCGGTG 933
DB 1109 GGGAGTATGTCGCAAGGCTGAACCTTAAAGGAATTTGACGGAAGGGCACCAGGAGTG 1168

QY 934 GATGATGTGGATTAAATTCGATGCAACGGGAAACCTTACCTGCTCTTGACATGTACGGA 993
DB 1169 GAGCCTGGCGCTTAAATTTGACTCAACACGGGGAATCTCACCAGGTCCAGACA-----C 1221

QY 994 ACTTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGAGTCTGCATGGCTGT 1053
DB 1222 AATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGGTGGTGGTGCATGGCCGT 1281

QY 1054 CGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCT----- 1106
DB 1282 TCTTAGTTGGTGGAGTATTTGCTGCTTAAATTCGATAACGAAACGAGACCTTAACCTAC 1341

QY 1107 TGTCAATAGTTGCCATCAATTTAGT-----TGGGCACTCTAATGACACTGCCGCTGACAAA 1161
DB 1342 TAAATAGTGGGTAGCAATTTGCTGGTATCCACTCTTTAGAGGACATATCGTTTCAAG 1401

QY 1162 CCGGAGGAAGGTGGGGATGAGCTCAAGTCTCATGCCCTT--ATGAGCAGGGCTTCACA 1219
DB 1402 CCGATGGAAGTTTGAGGCATTAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCGCGACG 1461

QY 1220 CGTCATACAAATCGGTACAGAGGTC---GCTAAGCGCGGAGTGGTGCAATCTCAT 1276
DB 1462 CGCGCTACACTGACGAGCGCAGGAGTCTAACCTTTGGCGGAGGCTTTGGTAACTTGT 1521

QY 1277 AAAAC--CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTCCGTTGAAGTCGATCGCT 1335
DB 1522 GAAACTCCGTCGTCTGGGGATAGAGCATTTGTAATTTATTTGCTCTTCAACAGGAATTCCT 1581

QY 1336 AGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCTTGTACACACCGCCCG 1395
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Db 1402 CCGATGGAAGTTTGGAGCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCGGCACG 1461
Qy 1220 CGTCATACAAATGGTTCGATACAGAGGTC---GCTAAGCCGCGAGGTGGTCCCAATCTCAT 1276
Db 1462 CGGCTACACTGACGAGGACGAGAGTCAACCTTGGCCGAGAGGCTTGGTAATCTTGT 1521
Qy 1277 AAAC-CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCT 1335
Db 1522 GAAATCCGTCGTGGGATAGAGCATTTGTAATTATTCTTCAACGAGGAATTCCT 1581
Qy 1336 AGTAATCGAGATCAGATCGTGGTGAATAGTTCCCGGGTCTTGTACACACCGCCG 1395
Db 1582 AGTAAGCGCAAGTCATCAGCTTGGCTTGTAGTCCCTCCCTTGTACACACCGCCG 1641
Qy 1396 TCACACCATGGGAGTGAGT 1414
Db 1642 TCCTAGTACCGATTGAAT 1660

RESULT 6

US-11-217-529-195591
; Sequence 195591, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195591
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195591

Query Match 8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;
Qy 649 CGTCAGAGGGGGTAGAAATTCGCGTGTAGCAGTGAATCGTAGAGATCGGAGGAATA 708
Db 869 CGGTGGGGGCATCAGTATTCAATTGTGAGAGTGAATTTCTGGATTATTGAAGACTA 928
Qy 709 CCATGCGCAAGGAGCCCTCGGGATGACACTGAGCTCATGTCACGAAGCGTGGGAG 768
Db 929 ACTACTGCGAAGCATTTGCCAAGGACGTTTCAATTAATCAAGAACGAAGTTAGGGAT 988
Qy 769 CAAACAGATTTAGATACCTCGGTAGTCCAGCCCTAAACGATGTCAATTAGCTGTTGGG 828
Db 989 CGAAGATGATCAGATCCGTCGTAGTTTAAACATAAATCTATGCCAGCTAGGATCGGT 1048
Qy 829 GTTTGAATCTTGGTAGCTAGCTAAACGCGTGAATTTGACCGCT-----G 874
Db 1049 GGTGTTTTTAAATGACCCACTCGGCACCTTACGAGAAATCAAGATCTTTGGTCTGGG 1108
Qy 875 GGAGTAGCGCCGCAAGGTTAAACTCAAGAGTAATTGACGG-GGACCCGACAAAGCGGTG 933
Db 1109 GGGAGTATGTCGCAAGGCTGAACCTTAAAGAAATTGACGGAAGGGCACCACGAGGATG 1168
Qy 934 GATGATGCTGATTAATTTGATGCAACGCAAGAAACCTTACCTCTTGTGATGTACGGA 993
Db 1169 GAGCTCGGCTTAATTTGATCTCAACACGGGAAACTCACGAGTCCAGACA-----C 1221

Qy 994 ACTTGTAGAGATATCTTGTGCCGCCGAAAGGAGCGGTAAACAGGTGCTGATGCTGT 1053
Db 1222 AATAAGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGTGTGGTGCATGCCGT 1281
Qy 1054 CGTCAGCTCGTTCGTCGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCTT----- 1106
Db 1282 TCTTAGTTGGTGGAGTGAATTTGTCTCTTAATTTGCGATAAACGAAACGAGACCTTAA 1341
Qy 1107 TGTCAATTAGTTGTCATCAATTTAGT-----TGGGCACTCTAATGAGACTGCCGTGACAA 1161
Db 1342 TAAATAGTGGTCTAGCATTTGCTGGTTATCACTTCTTAGAGGAGTATCGGTTCAAG 1401
Qy 1162 CCGAGGAAGGTGGGATGACGTCAAGTCTCATGCCCCTT--ATGAGCAGAGGCTTCACA 1219
Db 1402 CCGATGGAAGTTTGAAGCAATAACAGTCTGTGATGCCCTTAGACGTTCTGGCCCGCAG 1461
Qy 1220 CGTCATACAAATGGTGGTACAGAGGTC---GCTAAGCCGCGAGTGGTCCCAATCTCAT 1276
Db 1462 CGCGCTACACTGACGAGCCGAGTCTAACTTGGCCGAGAGGTCTTTGGTAACTTGT 1521
Qy 1277 AAAAC-CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCT 1335
Db 1522 GAAACTCCGTCGTGGGATAGACATTGTAATTTATTTGCTCTTCAACGAGGAATTCCT 1581
Qy 1336 AGTAATCGCAGATCAGCATGCTCGGTGAATAGCTTCCCGGGTCTTGTACACACCGCCG 1395
Db 1582 AGTAAGCGCAAGTCATCAGCTTGGCTTGTATAGTCCCTCCCTTGTACACACCGCCG 1641
Qy 1396 TCACACCATGGGAGTGAGT 1414
Db 1642 TCCTAGTACCGATTGAAT 1660

RESULT 7

US-11-217-529-195592
; Sequence 195592, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195592
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195592

Query Match 8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;
Qy 649 CGTCAGAGGGGGTAGAAATTCGCGTGTAGCAGTGAATTCGTAGAGATCGGAGGAATA 708
Db 869 CGGTGGGGGCATCAGTATTCAATTGTGAGAGTGAATTTCTGGATTATTGAAGACTA 928
Qy 709 CCATGCGCAAGGAGCCCTCGGGATGACACTGAGCTCATGTCACGAAGCGTGGGAG 768
Db 929 ACTACTGCGAAGCATTTGCCAAGGACGTTTCAATTAATCAAGAACGAAGTTAGGGAT 988
Qy 769 CAAACAGATTTAGATACCTCGGTAGTCCAGCCCTAAACGATGTCAATTAGCTGTTGGG 828
Db 989 CGAAGATGATCAGATACCGTCTAGTCTTAAACATAAATCTATGCCAGCTAGGATCGGT 1048

QY	829	GTTTGAATCCTTGGTAGCTAGCTAAACCGGTGAATTTGACCGCT-----G	874
Db	1049	GGTGTGTTTTTAATGACCCACTCGGCACCTTACGAGAAATCAAAAGTCTTTGGGTCTGGG	1108
QY	875	GGGAGTAGCGCGCAAGGTAAAACTCAAAGGAATTGACCG- GGACCGGCACAAAGCGGTG	933
Db	1109	GGGAGTATGGTCGAAGGCTGAAACTTAAAGAAATTTGACGAAGGACACACAGGAGTG	1168
QY	934	GATGATGTGGATTAAATTCGATGCAACGCGAAAAACCTTACCTGCTCTTTGACATGTACGGA	993
Db	1169	GAGCTCGGGCTTAATTTGACTCAACACGGGAAACTCACCCAGGTCCAGACA-----C	1221
QY	994	ACTTGGTAGAGATATCTTTGGTGCCCGAAGAGGACCGTAAACAGGTGCTGCTCATGGCTGT	1053
Db	1222	AATAAGGATTGACAGATTTGAGAGCTCTTTCTTTGATTTTGTGGGTGGTGCATGGCCGT	1281
QY	1054	CGTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCT-----	1106
Db	1282	TCTTAGTTGGTGGAGTATTTGCTGCTTAATTTGGTAACAAAGACCTTAACCTAC	1341
QY	1107	TGTCATTAGTTGCCATCATTTAGT-----TGCGCACTCTAATGAGACTGCCCGGTGCAAAA	1161
Db	1342	TAAATAGTGGTGTAGCATTTGCTGGTTATCCACTTCTTAGAGGACTATCGGTTTCAAG	1401
QY	1162	CGGAGGAAGTGGGATGACGTCAAGTCTCATGCGCCCTT--ATGACGAGGCTTACACA	1219
Db	1402	CCGATGGAAGTTTGAGGCAATAACAGGTCCTGTGATGCCCTTTAGACGTTCTGGGCGCGACG	1461
QY	1220	CGTCATCAATGTCGGTACAGAGGTC- --GCTAAGCGCGAGGTGGTGCAATCTCAT	1276
Db	1462	CGCGCTACACTGACGGACCGAGTCTAACCTTGGCCGAGAGGCTTGGTAAATCTTGT	1521
QY	1277	AAAAAC-CGATCGTAGTCCGATCGCACTCTCGCAACTCGAGTGCGTGAAGTCGGAATCGCT	1335
Db	1522	GAAACTCGTCTGGGGATAGAGCATTTGTAATTTATGCTCTTCAACGAGGAATTCCT	1581
QY	1336	AGTAATCGACATGACATGCTCGGTGAATACGTTCCGGGTCTGTACACACGGCCCG	1395
Db	1582	AGTAAGCGCAAGTCATCAGCTGCGTTGATTACGTCCTGCCCTTTGTACACACCGCCCG	1641
QY	1396	TCACACCATGGAGTGAGT	1414
Db	1642	TCGCTAGTACCGATTGAAT	1660
RESULT 8			
US-11-256-428-61			
; Sequence 61, Application US/11256428			
; Publication No. US20060095987A1			
; GENERAL INFORMATION:			
; APPLICANT: Niblett, Charles L.			
; TITLE OF INVENTION: Methods and Materials for Conferring Resistance to Pests and			
; TITLE OF INVENTION: Pathogens of Plants			
; FILE REFERENCE: VEN-100			
; CURRENT APPLICATION NUMBER: US/11/256,428			
; CURRENT FILING DATE: 2005-10-21			
; NUMBER OF SEQ ID NOS: 69			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 61			
; LENGTH: 1773			
; TYPE: DNA			
; ORGANISM: Artificial			
; FEATURE:			
; OTHER INFORMATION: Pratylenchus scribneri rDNA			
US-11-256-428-61			
Query Match 8.3%; Score 119.8; DB 7; Length 1773;			
Best Local Similarity 51.7%; Pred. No. 1.1e-30;			
Matches 408; Conservative 4; Mismatches 341; Indels 36; Gaps 5;			
QY	654	GAGGGGGGTAGAAATTCGCGTGTAGCAGTGAATCGTAGAGATCGGAGGAATACCGAT	713

Db	855	GGGGGCATTGCTATGCTACGTGAGAGTGAAATTTCTTGACCGCTAGCAAGACGAACTAC	914
QY	714	GGCGAAGGACCCCTTGGGATGACACTGACGCTCATGACGAAAGCTGGGAGCAAAAC	773
Db	915	AGCGAAGCAATTTGCCAAGAATGCTTTCATTAAATCAAGAAATGAGAGTTCAGAGTTCGAAG	974
QY	774	AGGATTAGATACCTGCTGTAGTCCACGCCCTTAAACGATGTCAATTTAGCTGTTGGGGTTTG	833
Db	975	GGCATAGATACCCCTTGTCTGACCGTAAACGATGCAATAGCAATAGCAKATCCCGCGGGG	1034
QY	834	AATCCTTTGGTAGCTAGCTAACGCGTGAAATTT-----GACCGCTGGGGAGTA	881
Db	1035	AATCTTGCCCTGGTGGGAGCTTCCCGGAAACGAAAGTCTTCCGGTTCCGGGGAAAGTA	1094
QY	882	CGGCGCAAGGTTAAACTCAAAGGAATTGACGG- GGACCGGCACAAAGCGGTGATGATG	940
Db	1095	TGGTTGCAAGCTGAAACTTTAAAGGAATTGACGGAAGGACCACCAGGAGTGGAGCGCTG	1154
QY	941	TGGATTAAATTCGATGCAACCGGAAACCTTTACTGCTCTTGACATGTACGGAACCTTGGT	1000
Db	1155	CGGCTTAATTTGACTCAACACGGGAAACTCACCCGCCCGGACACCGTAAGGATTGCA	1214
QY	1001	AGAGATATCTTGGTGGCCGGAAGGAGCGCTAAACACAGGTGCTGCAATGGTGTGTCAGC	1060
Db	1215	GATTGATAGCTTTTTCATGATTCCGGT-----GATGGTGGTGCATGGCCGTTCTTAGT	1267
QY	1061	TCGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTT-----G	1108
Db	1268	TCGTGGAGCGAATTTGCTGGYTTATTCGATAACGAGCGAGACTCTGGCCTACTTAAATAG	1327
QY	1109	TCATTAGTGCATCATTTAGTTGGGCACCTTAATGAGACTGCCGGTGACAAAACCGGAGG	1168
Db	1328	TCGGCGAATGCTCTCTGTGTCATGACTTCTTAGAGGGAATTTGCGTGTTCAGCGCGACG	1387
QY	1169	AAGTGGGGTAGCGTCAAGTCTCTCATPGGCCCTTATGACAGAGGCTTACACGTCATACA	1228
Db	1388	AAATTGAGCAATAACAGGCTGTGTGATGCCCTTAGATGTCGGGGCTGCACGCGCTACA	1447
QY	1229	ATGCTCGGTACAGAGGTCGCTAAGCCGCGAGTGG-----TGCCAATCTATAAAACCGA	1284
Db	1448	CTGSCAAAATCAGCGTCTTGTCTCTCCGAAAGGAGTTGGTAAACCATTTGAAAAATTTG	1507
QY	1285	TCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCTAGTAATCGC	1344
Db	1508	CCGTGATTGGATCGGAAATTCGAATTTATTTTCGTGACAGGGAATTCCAAGTAAGTGC	1567
QY	1345	AGATCAGCATGCTGCGGTGAATAGTTCCTCGGGTCTTTGTACACACCGCGCTCACCAT	1404
Db	1568	GAGTCATCAACTCGCGTTGATTACGTCCCTTGCCCTTTGTACACACCGCGCTCGCTGCC	1627
QY	1405	GGGAGTGAG	1413
Db	1628	GGGACTGAG	1636
RESULT 9			
US-11-284-877-16			
; Sequence 16, Application US/11284877			
; Publication No. US20060095984A1			
; GENERAL INFORMATION:			
; APPLICANT: Hadlaczky, Gyula			
; Szalay, Aladar			
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS			
; NUMBER OF SEQUENCES: 34			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: Fish & Richardson			
; STREET: 12390 El Camino Real			
; CITY: San Diego			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 92130			
; COMPUTER READABLE FORM:			

MEDIUM TYPE: CD-ROM
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/284,877
FILING DATE: 21-Nov-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/808,689
FILING DATE: 24-MAR-2004
APPLICATION NUMBER: 10/219,694
FILING DATE: 14-AUG-2002
APPLICATION NUMBER: 10/151,081
FILING DATE: 16-MAY-2002
APPLICATION NUMBER: 10/151,078
FILING DATE: 16-MAY-2002
APPLICATION NUMBER: 10/125,767
FILING DATE: 17-APR-2002
APPLICATION NUMBER: 10/287,313
FILING DATE: 01-NOV-2002
APPLICATION NUMBER: 09/799,462
FILING DATE: 05-MAR-2001
APPLICATION NUMBER: 09/724,872
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 09/724,726
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 09/724,693
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 17084-004018/4020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-678-4777
TELEFAX: 202-626-7796
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2218 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-284-877-16

Query Match 7.2%; Score 103.2; DB 7; Length 22118;
Best Local Similarity 50.9%; Pred. No. 1.9e-24;
Matches 408; Conservative 0; Mismatches 348; Indels 46; Gaps 5;
QY 649 CGTCAGAGGGGGTAGAATTCGCCGTGTAGCAGTGAATCGGTAGAGATGCCGAGGAATA 708
DB 10570 CGGCCGGGGCATCTGATTCGCCCGCTAGAGTGAAATCTTGGACCGCGCAACGCG 10629
QY 709 CCGATGGCGAGGAGCGCCCTCGGATGACACTGACGCTCATGCAGAAAGCGGTGGGAG 768
DB 10630 ACCAGAGCGAAAGCATTTGCCAAGAATGTTTTCATTAAATCAAGAACGAAAGTCGAGGTT 10689
QY 769 CAACAGGATTAGATACCTCGGTAGTCCAGCCCTAAACGATGCTAATAGCTGTTGGG 828

Db 10690 CGAAGACGATCAGATACCGTCGTAGTTCGAGCATAAAGATGCCGACGTGGCGATCGGC 10749
QY 829 GTTTGAATCTTGGTAGCGTAGCTAACGCGTGAATTTGACCG-----CCTG 874
Db 10750 GGGCTTAATCCCATGACCCCGCGGAGCTTCGGGAAACCAAAAGTCTTTGGGTTCCGG 10809
QY 875 GGGAGTACGGCCGCAAGGTTAAAACTCAAAGGAATTTGACGGGACCCGCAACAGCGGTGG 934
Db 10810 GGGAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTTGACGGAAGGACACCACCAGGAGTG 10869
QY 935 ATGATGTGATTAATTCGATGCAACCGGAAACCTTACCTGCTCTTGACATGTACGGAA 994
Db 10870 GGCCTCGGCTTAATTTGACTCAACACGCGGAAACCTTACCCGCGCGGACACGACAGGA 10929
QY 995 CTTCGTAGAGATATCTTCGTGCCCCGAAAGGGAGCCGCTAAACACAGGTGCTCATGGCTGTC 1054
Db 10930 TT-----GACAGATTGATGCTCTTTCGATTCGGTGGTGGTGGTGCATGGCGTT 10982
QY 1055 GTCAGCTCGTGTGAGATGTTGGTTAAAGTCCCGCAACGACGCGCAACCCCTTG----- 1108
Db 10983 CTTCGTGTTGGAGCGATTTGCTGTTAAATTCGATAACGAACGAGACTCTCGCATGCT 11042
QY 1109 ----TCATTAGTTGCCATCATTTAGTTGGGCACTC-----TAATGAGACTGCGGT 1155
Db 11043 AACTAGTTACGCGACCCCGAGCGGTGCGCGTCCCCCACTTCTTAGAGGGAACAAGTGC 11102
QY 1156 GACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCATGGCCCTTATGAGCAGGCTT 1215
Db 11103 GTTCACCCACCGAGATTGAGCAATTAACAGTCTGTGATGCCCTTAGATGTCGGGGCTG 11162
QY 1216 CACAGCTCATACAATGGTTCGTAAGAGGGTTCGTAAGCGCGC-----AGGTGGTGCCA 1269
Db 11163 CACGGCGCTACACTGACTGGCTCAGCGTGTGCTTACCTTCCGCGGAGCGCGGTAA 11222
QY 1270 ATCTATAAAACGATCGTAGTCCGATCGACTCTGCAACTCGAGTGGTGAAGTCGA 1329
Db 11223 CCCGTTGAACCCCACTTCGTGATGGGATCGGGATTCGCAATTAATCCCATGAACGAGGA 11282
QY 1330 ATCGCTAGTAATCGCAGATCAGCATGCTCGGTGAATAGTTCCTCCGGGTCTTCTACAC 1389
Db 11283 ATTCCAGTAAGTGGGTCTAAGTTCGTTGATTAAAGTCCCTGCCCTTTGTACAC 11342
QY 1390 CGCCGTCACACCATGGGAGTG 1411
Db 11343 CGCCGTCGCTACTACCGATTG 11364
RESULT 10
US-10-511-937-333
; Sequence 333, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2

Matches	421;	Conservative	0;	Mismatches	335;	Indels	49;	Gaps	8;
Qy	649	CGTCAGAGGGGGGTAGAAATTC	CGCGGTGTAGCAGTGA	AAATCGT	TAGAGATG	CGGAGGAATA	708		
Db	4583	CGGCGGGGGGCAATTCGTAATTT	TCGCGCGGTAGAGGTG	AAATTTCTTGGA	CCGCGCAAGACGG	4642			
Qy	709	CCGATGCGAAGGCGAGCCCTCG	TGGATGACACTGACGCT	CATGAC	CAAGAAACGTCGGGGAG	768			
Db	4643	ACACAGCGAAAGCATTTTGCC	AGATGTGTTTCAATTAAT	CAAGAACGAAATGCGGAGTT	4702				
Qy	769	CAAAACAGGATTAGATACCTCT	TGTAGTCCAGCCCTTAAAC	GATGTCAATTAAGCTGT	TTCGGG	828			
Db	4703	CGAAGACGATCAGATACCGTCT	GATGTTCCGACCAATAAAC	GATGCCGACCGCGATGCGC	4762				
Qy	829	GTTTGAATCCTTGGTAGGTAGCT	TAAACGCGTGAATTTGACCG	-----CCTG	874				
Db	4763	GGCGTTATTCCTATGACCGCG	CGCGGACGCTTCGCGGAAAC	CAAGTCTTTGGGTTC	CGGG	4822			
Qy	875	GGGAGTACGGCCGCAAGGTTAA	AAACTCAAAGGAATTGACG	G-AGCCCGCACAAAGCGGTG	933				
Db	4823	GGGAGTATGGTTGCAAGCTCA	AACTTAAGGAATTCACGGA	AGGACCAACGAGATG	4882				
Qy	934	GATGATGTGGAATTAATTCGAT	GCACCGGAAAAACCTTAC	CTGCTCTTGACATGTACGGA	993				
Db	4883	GAGCCTCGGGCTTAATTTGACT	CAACACGGGAAACCTCAC	CCGCGCCCGGACACGACAGG	4942				
Qy	994	ACTTGGTAGAGATATCTTTGGT	GGCCGAAAGGAGCCGTAA	CACAGGTGCTGCAATGCTGT	1053				
Db	4943	ATT-----GACAGATTGAT	AGTACTTTTCTCGAATCCG	TGGGTGGTGCATGCGCCGT	4995				
Qy	1054	CGTCAGCTCGTGTGCGTAGAT	TGTTGGGTAAAGTCCCG	CAACGACGCGCAACCCCTTG	-----1108				
Db	4996	TCTTAGTTGGTGGAGCATTTGT	CTGTGTTAATTCGATAACGA	ACGAGACTCTGCGCATGC	5055				
Qy	1109	-----TCATTAGTTGCCATCA	TATTAGTTGGGCACTC-----	TAATGAGACTGCGCGG	1154				
Db	5056	TAACTAGTTACGACACCCGAG	CGGTGCGCGTCCCCCAACT	TTCTTAGAGGGACAAGTGG	5115				
Qy	1155	TGACAAACCGGAGGAAGTGGG	GATACGTCAAAGTCTCAT	TGGCCCTTATGACAGGCT	1214				
Db	5116	CGTTCAGCCACCGAGATTGAC	GCATTAACAGGCTCTGTGAT	GCCCTTAGATGTCGCGGCT	5175				
Qy	1215	TCACAGTCAACAATGGTCGGT	ACAGAGGT-----CGCTAA	CGCGAGGTGGTGCCA	1269				
Db	5176	GCACGCGCGTACACTGACT	GGCTACGCTGTGCCTAC	CTCCCTAGCCGCGAGCGCGGTA	5235				
Qy	1270	ATCTCAAAAAACGA-TCGTAG	TCCGATCGCACTCTGCAACT	CGATGCGTGAAGTCGG	1328				
Db	5236	ACCGTTGAACCCCATTCGTGAT	GGGGATCGGGATTGCAATTA	TATCCCATGAACGAGG	5295				
Qy	1329	AA---TCGCTAGTAATCCGAGAT	CAGCATGCTGCGGTGAAT	CAGTTCCCGGCTCTTTGTACA	1386				
Db	5296	GAATCCCGAGTAAGTCGGGT	CATAGCTTGGTGTGATTAG	TCTCCTCGCCCTTTGTACA	5355				
Qy	1387	CACGCCCGTCAACACATGGAG	TG 1411						
Db	5356	CACGCCCGTCGTACTACCGAT	TG 5380						

RESULT 12

US-11-217-529-166170
; Sequence 166170, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

```

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 137023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166170
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166170

```

Query Match	2.88;	Score 40;	DB 7;	Length 600;
Best Local Similarity	56.78;	Pred. No. 0.00044;		
Matches 93;	Conservative 0;	Mismatches 70;	Indels 1;	Gaps 1;
Qy	221	AGCCGAGCTCTGATTAGCTAGTGGTGAGGTACACCAAGGCGGCGATCAGTAGC	280	
Db	428	AGCCATAATGCTTTAGGTAGTGGTTTAAATAAAGTGAACCTTAGCCAAAGATCCATAAT	487	
Qy	281	GGGTCTGAGAGGATGATCCGCCACACTGGGAGTGAGACACGGCCGAGACTCTTAGGGGAG	340	
Db	488	CGATAATGAAGTTAGAAGC-ATCACGTTGACTCTGAAATATAGTCAATATCTATATGAT	546	
Qy	341	GCAGCAGTGGGGAAATTTTGGACAATGGGGCAACCTTGATCCAG	394	
Db	547	ACAGCAGTGAAGGAATATTGCAACAATGATCGAAAGATTGATCCAG	590	

RESULT 13

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US-11-217-529-166173
; Sequence 166173, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166173
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166173

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	Query Match	2.8%	Score 40;	DB 7;	Length 600;
	Best Local Similarity	56.7%;	Pred. No. 0.00044;		
	Matches 93;	Conservative	0;	Mismatches 70;	Indels 1; Gaps 1;
Qy	221	AGCCGAGCTGCTGATTAGCTAGTTGGTGAGGTAAGAGCTCACCAAGCGGACGATCAGTACG 280			
Db	93	AGCCAATATGGTTTTAGTTAGTAGTGGTTTTAATAAAGTGAACCTAGCCACGATCCATAAT 152			
Qy	281	GGGTCTGAGAGGATGATCCGCCACACTGGGACCTGAGACACGGCCGACACTCTTACGGGAG 340			
Db	153	CGATAATGAAGTTAGAACG-ATCACGTTGACTCTGAAATATAGTCAATATCTATATGAT 211			
Qy	341	GCAGCAGTGGGGAAATTTTGACAATGGGGCAACCCCTGATCCAG 384			
Db	212	ACAGCAGTCGAGGAATATTGACAATGATCGAAAGATTGATCCAG 255			

RESULT 14

US-10-488-619-1
; Sequence 1, Application US/10488619

